

STIC-Biotech/ChemLib

71738

From:
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Subject:

Collins, Cynthia
Wednesday, 4/24/2002 4:59 PM
STIC-Biotech/ChemLib
sequence search request SN 09/828447

Please search, both prior art and interference, for SN 09/828447:

1) SEQ ID NO:12
2) SEQ ID NO:7

Thank You,

Cynthia Collins
Art Unit 1638
CMI, 9A12 (office) or 9E12 (mailbox)
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Edward Han
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

4/6/01
prev 4/7/00
1026 4/7/99

TYPE OF SEARCH:

NA Sequences: ☒
AA Sequences: ☒
Structures: ☒
Bibliographic: ☒
Litigation: ☒
Full text: ☒
Patent Family: ☒
Other: ☒

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.: ☒
WWW/Internet:
Other (specify):

Searcher:
Phone:

Location:

Date Picked Up:

Date Completed:

Searcher Prep/Review:

Clerical:

Online time:

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 26, 2002, 13:07:56 ; Search time 2533.87 Seconds

(without alignments)
11393.634 Million cell updates/sec

Title: US-09-828-447-7

Perfect score: 2139

Sequence: 1 atccgggcttcgggagttt.....gtgaccccaaggtaacgcc 2139

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_esti:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	298.8	14.0	419	10	BJ194081
2	284.8	13.3	496	9	AW561280
3	281.2	13.1	706	10	BJ167090
4	251.2	11.7	540	10	BJ163593
5	183	8.6	551	10	BJ206977
6	181.6	8.5	543	10	BJ160350
7	176.2	8.2	659	10	BJ160350
8	173.2	8.1	783	10	BJ265786
9	171.6	8.0	775	10	BG646260
10	167.2	7.8	617	9	AW277493
11	163.4	7.6	772	10	BE822903
12	156.8	7.3	606	9	AW938235
13	156.2	7.3	838	9	AW448540
14	155	7.2	527	10	BG381790
15	154.2	7.2	655	10	BF637852
16	152.4	7.1	421	9	AW496918
17	149.4	7.0	716	10	BG644550

18	147.6	6.9	871	9	BE040051
19	145	6.8	716	10	BG645186
20	141	6.6	757	10	BI177154
21	138	6.5	586	9	AW561394
22	136	6.4	805	10	BI920569
23	135.8	6.3	761	10	BI969233
24	134.8	6.3	589	9	AV536140
25	133.6	6.2	628	9	AW774900
26	130.4	6.1	589	9	BE036525
27	130.4	6.1	764	9	BI794656
28	128.8	6.0	582	9	AW564895
29	126.6	5.9	607	9	AW164281
30	126	5.9	635	9	AW108535
31	125.8	5.9	455	10	BJ175092
32	123.8	5.8	646	10	BG595391
33	119.8	5.6	493	10	BF069301
34	119.6	5.6	496	10	BJ192301
35	119	5.6	477	10	BJ193355
36	116.6	5.5	397	10	BG137605
37	115.6	5.4	823	10	BF267475
38	114	5.3	649	9	AW685378
39	113.8	5.3	557	9	AW257926
40	111.8	5.2	597	9	AI485566
41	107.8	5.0	436	9	AI948076
42	107.6	5.0	554	9	AW735896
43	107.4	5.0	615	10	BG136556
44	106	5.0	681	9	AW774123
45	105.2	4.9	555	10	BI699487

ALIGNMENTS

RESULT 1

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BJ194081 419 bp mRNA linear EST 24-JAN-2002
BJ194081 normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata Physcomitrella patens subsp. patens cDNA clone pphnlh22 5', mRNA sequence.
BJ194081
BJ194081.1 GI:18362014
EST.
Physcomitrella patens subsp. patens.
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariaceae; Funariales; Funariaceae; Physcomitrella.
1 (bases 1 to 419)
Fujita, T., Shin-i, T., Seki, M., Kamiya, A., Uchiyama, I., Nishiyama, T., Carninci, P., Hayashizaki, Y., Shinozaki, K., Kohara, Y. and Hasebe, M.
Comparison of the moss Physcomitrella patens genome with flowering plants genome
Unpublished (2002)
Contact: Tadashi Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-8855
Email: tshini@genes.nig.ac.jp
A backbone of the vector is pBluescript II, that was in vivo excised from a modified LPS phage vector (Mo bi Tec, Germany). XhoI digested-5' end of cDNA is ligated to SalI site of the vector, and the BamHI digested-3' end including poly-A tail is ligated to BamHI site of the vector. cDNA insert could be amplified with conventional T7 and T3 primers. This normalized full-length cDNA library was generated basically according to the method described in Genome Research 10, 1617-1630 (2000), Carninci, P. et al. Protonemata were blended by the POLYTRON, and then cultivated on the BCD medium containing 1mM NAA (naphthalene acetic acid) for 8 to 11 days under the continuous light.

FEATURES

Location/Qualifiers

1..419

Query Match 14.0%; Score 298.8; DB 10; Length 419;
 Best Local Similarity 99.0%; Pred. No. 1.3e-74;
 Matches 311; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 /organism="Physcomitrella patens subsp. patens"
 /db_xref="taxon:145481"
 /clone="pbn1h22"
 /clone_lib="normalized full length cDNA library,
 chloronemata, caulonemata and rhizoid-like protonemata"
 /tissue_type="mixture of chloronemata, caulonemata and
 rhizoid-like protonemata"
 BASE COUNT 96 a 75 c 145 g 103 t
 ORIGIN

Qy 7 ggtctggaggttaagagatgtccacggtgtgggaagacgagcggtgtatcaggtttg 66
 Db 106 GACTTCGGGAGTTTAAGAGGATGTCAGCGGTGGGAAGACGAGCGGTGTATCAGGTTG 165
 Qy 67 ggtgagacttaagttgacgaggtgtaaggatgcggtctgctcactgggtttgcaaaatgt 126
 Db 166 GTTGAGGCTTAAAGTTGACGGAGTGTAAAGGATCGGCTCGTCTACCTGGTTTCAAAATGT 225
 Qy 127 gtctcatagcatgtgtcgaagtgggaaccccaagggatccgagagcaagacctggt-g 185
 Db 226 GTTCCATAGCATGTTGTGNAAGTGGAAACCCCGAAGGGGATCCGGAGCAAGACCTGGTGG 285
 Qy 186 ggggaggtgtcacatatatagcggagaaatgagagatgagtcgaggggtgtctgaaa 245
 Db 286 GGGGAGGTGTTCACATATATACAGCGAGATGAGAGAAATGAGTGGCGGAGGTGTCTGAAA 345
 Qy 246 ttcttcacacagacaaagggatgtcgaacttcaccttgatgcgcgaagcagatcatg 305
 Db 346 TTCTTCATACAGCAAGGGATGTCGACTTCACCTTGATGAGCCCAAGCAGATCATG 405
 Qy 306 gaggcattcgcaa 319
 Db 406 GAGCGCATTCGCAA 419

RESULT 2

AW561280 496 bp mRNA linear EST 08-MAR-2000
 LOCUS ga78a1.y1 Moss EST library PPU Physcomitrella patens cDNA clone
 DEFINITION PEP SOURCE ID: PPU140521.5, similar to TR:Q43442 Q43442
 PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C P12.1, mRNA sequence.

ACCESSION AW561280
 VERSION 1
 KEYWORDS EST
 SOURCE Physcomitrella patens.
 ORGANISM Physcomitrella patens

REFERENCE
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
 1 (bases 1 to 496)
 Quatrano, R., Bashardes, S., Cove, D., Cuming, A., Knight, C., Clifton
 S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood
 K., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T.,
 Steptoe, M., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
 Waterston, R. and Wilson, R.
 Leeds/Wash U Moss EST Project
 Unpublished (1999)

TITLE
 JOURNAL
 COMMENT
 Contact: Ralph Quatrano
 Leeds/Wash U Moss EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

Libraries were constructed by Dr. Stavros Bashardes as part of the
 Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
 Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
 University Genome Sequencing Center For information on obtaining a
 clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)

Seq primer: -40RP from Gibco
 High quality sequence stop: 309.
 Location/Qualifiers
 1. 496
 /organism="Physcomitrella patens"
 /db_xref="taxon:3218"
 /clone="PEP_SOURCE_ID:PPU140521"
 /clone_lib="Moss EST library PPU"
 /tissue_type="protonemata: 7 day old tissue
 ammonium-grown"
 /lab_host="DH10B"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI; Construction of the cDNA library was carried out
 using Strategenes 'UnizAP - cDNA synthesis kit'. cDNA
 was constructed using an oligo dt primer/linker that
 contains a XhoI site within it. Following ds cDNA
 synthesis, EcoRI adapters were ligated to the blunt ends
 and sample was digested with XhoI. The result is cDNA
 with an EcoRI sticky end on one side and a XhoI sticky
 end on the other. This cDNA was ligated directionally in
 UnizAP arms. The vector is designed containing the
 pBluescript sequence as well as lambda DNA and cDNA is
 cloned within this pBluescript sequence. The vector was
 then packaged using Gold gigapackaging extracts. Library
 was grown in XL1Blue MRP cells and amplified. The library
 was excised by mass excision using Strategenes 'Mass
 excision kit' that uses exassit as a helper phage that
 releases the pBluescript sequence and circularises it as
 single stranded plasmids that are then packaged (by helper
 phage) and secreted out of the host cell as phagemids.
 SOLR cells were transformed with phagemids and the library
 was plated out on LB-amp plates to select for
 transformants. Approximately 1,000,000 colonies were grown
 and recovered. The double stranded plasmid library was
 recovered by using Quiagen Midi prep kit. 2 micro grams of
 each library were used to transform DH10B cells by
 electroporation."

BASE COUNT 148 a 105 c 126 g 117 t
 ORIGIN

Query Match 13.3%; Score 284.8; DB 9; Length 496;
 Best Local Similarity 73.4%; Pred. No. 1.5e-70;
 Matches 364; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

Qy 1454 gctttggcaggcatttgcaagttcaagggaatggggatgtgggtatgttttgaagcc 1513

Db 1 GCTCTGGCAAGCCACCGCAAGTTCAGGGGAATGGTGGCTGTGATACATCCTTAAGCC 60

Qy 1514 acagtatctgttgaaacttgccttctgtgtgctttcaaccacacatcacccagaaa 1573

Db 61 AAAGTATCTATTGGAAGATTGGCCCATGTAACCTTTTAACCTTCAGCTCCTGGAGA 120

Qy 1574 cacaaccttaattcaagattaaagtattgaactctgggagtggaacagccttttc 1633

Db 121 TACAAGATGATCTTGAAGTAAAGGTAATACAGACCATGGGATGGACAAAAGCGTTCC 180

Qy 1634 caaacgccatttgacattctcaccctccagattcttcactaggtgtgtgtgtgtgtg 1693

Db 181 CAATACCATTTCAACCTTTTACCTCGCTCCAGATTCTTCACTAGGTGCTGTGACTGG 240

Qy 1694 agtgcctgctgacgagggcccaagtgggaagacatctgtgtgtggacaatttcaggccccc 1753

Db 241 AGTGCCTGCCGATGTGGCAAAAGTGGAATCTCCGTTATAGATGACATTTGGGAACCCCA 300

Qy 1754 ttggaatgagaccatgagtttgccttaaatgcccctgagctgcactactctgcacatga 1813

Db 301 CTGGAACGAGGATCACAGGATTATACCTGAATGCCCTGAACCTTGACATGCTCCGAATGA 360

Qy 1814 ggtccgagacatgatgatgacaaagatgagtttaagggcagacatgccttcccat 1873

Db 361 AGTTAGAGATCAGCAGGAGAAAGTCAAGATGATGTCGAAGGGCATGCTGCTTCCAAT 420

Db	586	TGGGCAAAAGCGTTCCCAATACCATTTTCGCTTCGCTCCAGATTTCTTCACT	527
Qy	1677	aggggtgattggtgggagtcgctgacagcgaagtggaagacacatctgtggtggac	1736
Db	526	AGGCTGCTTGTGACTGGAGTGCCTCCGATGTGCAAAAGTGGAAACATTCCTGTTATAGAT	467
Qy	1737	aattcatggcaccattggaatgagaccatgattgcttgccttaaaatccctgagctc	1796
Db	466	GACGTTTGGGAACCCACTGGAACGAGGATCAGGAGTTTACCTTAATGCCCTGAACCT	407
Qy	1797	gcactacttcgactgaggttcgcagaccatgatgatgatacaagatgagtttgagggg	1856
Db	406	GCATGCTCCGAATTAAGTTAGAGTACAGCAGGAGGAAAGTCAAGATGAGTTCGAAGG	347
Qy	1857	cagacatgcttccatccatccatgagtcgagtcgggagtcgctgcatcaaatgacac	1916
Db	346	CAGCGGTGCTTCCATGTCATGAATTAAGAGCGGCTATCGATGCTGCAGATGTATGAC	287
Qy	1917	aagaaggcgaatgactgaaagcgctgctgattgtttcattcttcaaaa	1966
Db	286	AAAAAGGCGAGTGTGTGAAGGCGTGCAAAATGTTGTTCCATTTTCAAAA	237
RESULT	4		
LOCUS	BJ163593	540 bp	linear
DEFINITION	BJ163593	full length cDNA library, chloronemata and young gametophores	Physcomitrella patens subsp. patens cDNA clone
ACCESSION	BJ163593		
VERSION	BJ163593.1	GI:18331582	
KEYWORDS	EST.		
SOURCE	Physcomitrella patens subsp. patens.		
ORGANISM	Physcomitrella patens subsp. patens		
REFERENCE	1	(bases 1 to 540)	
AUTHORS	Fujita, T., Shin-i, T., Seki, M., Kamiya, A., Uchiyama, I., Nishiyama, T., Carninci, P., Hayashizaki, Y., Shinozaki, K., Kohara, Y. and Hasebe, M.		
TITLE	Comparison of the moss Physcomitrella patens genome with flowering plants genome		
JOURNAL	Unpublished (2002)		
COMMENT	Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855		
FEATURES	1	.706	
source	/organism="Physcomitrella patens subsp. patens"		
	/db_xref="taxon:145481"		
	/clone="pphi4a15"		
	/clone_lib="full length cDNA library, chloronemata and young gametophores"		
	/tissue_type="mixture of chloronemata and young gametophores with 2 to 5 leaves"		
BASE COUNT	188 a	175 c	200 t
ORIGIN			
Query Match	13.1%	Score 281.2	DB 10; Length 706;
Best Local Similarity	74.9%	Pred. No. 2.1e-618	Indels 0; Gaps 0;
Matches	352; Conservative	0; Mismatch 118;	
Qy	1497	gggtatgtttgaagccacagatctgttgaaactgcttctggtgcttccttcaac	1556
Db	706	GGATACATCTTAAGCCAAAGTATCTATTGGAGATTTCGCCAATGGTAAACCTTTTAAAC	647
Qy	1557	cccatcaccggaacacaccccttaattctcaagattataagttatgactaccttgga	1616
Db	646	CCTTCAGCTCTGGAGATACGAAGATGATCTTGAAGGTAAGGTAATGACCAACCTGGGA	587
Qy	1617	tgggacagggccttttccaaacccattttgacctattctcattccacgttcttcaact	1676

Center For Genetic Resource Information

National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp

A backbone of the vector is basically from pBluescript(KS), that was in vivo excised from a modified lps phage vector (Mo bi Tec, Germany). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector. cDNA insert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated basically according to the method described in The Plant J 15, 707-720 (1998) Seki M. et al. Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13-14 days under the continuous light.

FEATURES

Location/Qualifiers
1. 543
Source

/organism="Physcomitrella patens subsp. patens"
/db_xref="taxon:145481"
/clone="pph18m12"
/clone_lib="full length cDNA library, chloronemata and young gametophores"
/tissue_type="mixture of chloronemata and young gametophores with 2 to 5 leaves"

140 a 103 c 171 g 129 t

BASE COUNT
ORIGIN

Query Match 8.5%; Score 181.6; DB 10; Length 543;
Best Local Similarity 67.5%; Pred. No. 8.4e-41;
Matches 286; Conservative 0; Mismatches 134; Indels 4; Gaps 2;

QY 80 gttgacggagtgaaggatcggttcgctcactgggtttgcaaaatgtgtccatgcatg 139
|||||
Db 120 GGTGTCGGAGGGGATTTATTGTGCCGTAGTGGTGTTCGAAATGTGTCTATTCCGTT 179

QY 140 ttgtcaagtgaaccgcaaggatccgagcaagacctggtgggaggtgttcac 199
|||||
Db 180 CGGTCCGAGAGAGTCCCAAGAGGGGATTTGGCCGAGGATCTATTGGGGATGTGTTCTC 239

QY 200 aatatacagcagaatgagaggtgagtcgaggggttgctgaaattcttgcatacaga 259
|||||
Db 240 GACTTACAGCGAGATGGGAAGTGGACGCGAGGGGTGCTGAAATTTCTTGACAGACAGA 299

QY 260 gcaagggtggtcgtactcccttgatgacgccaagcagagatcatggcgcatctgcaa 319
|||||
Db 300 GCAAGGGGATAGCAAGTCTCTCTAGATGACGCCCAAGCATTTAGTGGAGTTGATTCGGAA 359

QY 320 ggaatgaagaatc---cttcggactcgctctatcaactcagacttgcgaaggagc 376
|||||
Db 360 TGAAGACATAGTCGNAATTCCTGGGTTCATCGTCAGCTCGGACTGTCGAAGGGTGA 419

QY 377 ttttcggaatgactgatgaatcccgactgaatggcgttettacacacggttgcaccca 436
|||||
Db 420 TTTTAAAAACTATGCTACTGAGCCGGATTTGAATGGGGTTCCTTGAAGACACTGTGCATCA 479

QY 437 agacataccag-cgatctccactatttcattatcacgcccataactcgtactcga 495
|||||
Db 480 AGACATGACGAGCCCGTATTGCGACTACTTCATATTCACTGTGTGACAACTCGTACTTGA 539

QY 496 ccgg 499
|||
Db 540 CGGG 543

RESULT 7

BI265786 659 bp mRNA linear EST 18-JUL-2001
LOCUS NF095B12IN1F1101 Insect herbivory Medicago truncatula cDNA clone
DEFINITION NF095B12IN 5', mRNA sequence.
ACCESSION BI265786
VERSION BI265786.1 GI:14869341

KEYWORDS

SOURCE
ORGANISM

EST.
barrel medic.

Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

REFERENCE 1 (bases 1 to 659)

AUTHORS Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Iman, J.T., Weller, J.W. and May, G.D.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library
JOURNAL Unpublished (2000)
COMMENT Contact: Korth K

Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701, USA
Tel: 501 575 5191
Fax: 501 575 7601
Email: korth@comp.uark.edu

Insert Length: 659 Std Error: 0.00

Plate: 095 ROW: B column: 12

Seq primer: TCACAGAGAAACAGCTATGAC.

Location/Qualifiers

1. 659

/organism="Medicago truncatula"

/db_xref="taxon:3880"

/clone="NF095B12IN"

/clone_lib="insect herbivory"

/tissue_type="local and systemic leaves"

/dev_stage="mature"

/note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

BASE COUNT 199 a 106 g 149 g 191 t 14 others

ORIGIN

Query Match

8.2%; Score 176.2; DB 10; Length 659;

Best Local Similarity 55.5%; Pred. No. 3.4e-39;

Matches 325; Conservative 0; Mismatches 261; Indels 0; Gaps 0;

QY 1282 tggaaaaagtgtgaaaaagtggccgaagctctgttcaaaatccacgagaagaacattt 1341
|||||
Db 74 TTGAAAAGGCTGCTGAACATACGGAAGAAATTTGCAGGTTCACTCAGCAGAATATAT 133

QY 1342 tacgtgttactctgctgaatcgttaactcctcaactctgcctactctggtt 1401
|||||
Db 134 TCGAGTGTATCCGAAAGGTACACGCATTCCTCAATAATTAATCCATTAATTTGGGT 193

QY 1402 ggaactacggagctcaaatggtgctcaaaacatcagggctatggttaagagctttggc 1461
|||||
Db 194 GGATGATGGAGCTCAGATGTTGTCATTTAATGTCANGTTATGGANATCTCTTTNGT 253

QY 1462 aggcatttggcgaattcgaaggaaatgggggatgtgggtatgttttgaagcacaagtc 1521
|||||
Db 254 TGATGCAAGGAATGTTNAAAGCAATGGAGTGGGTGTTTGTAAAAACANATTTTC 313

QY 1522 ttttggaaaaactgcttctgtgcttcaaccacacatcccccacacacacacccc 1581
|||||
Db 314 TATTAAAAACTCGTCCCAATATGAGATTTTCNATCTTAAGCTAATTTGGCATCGAAA 373

QY 1582 taattctcaagattaaagtattgactactccttgggatgggacaagccttttccaacgcc 1641
|||||
Db 374 CTACITTTGAAGGTGACTGTATACATGGGAGAAGGATGTTATGATTTCAAGCATACAC 433

QY 1642 atttgacctattctcaacctccagatttctcactagggtgattgttggtggagtcctg 1701
|||||
Db 434 ATTTGATCAGTCTCACCCTCCAGACTTCTATGCAAGGGTGGAAATCGCTGGAGTCCCTT 493

QY 1702 ctgacgagcccaagtggaagacatctgtgttgacacatctgtgttgacacatctggtg 1761
|||||

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE
AUTHORSTITLE
JOURNAL

COMMENT

1 (bases 1 to 772)
Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Coryell, V., Erpelting, J., Rapp, C., Shoop, E., Pardin, J., Liu, L., and Lewin, H. A Functional Genomics Program for Soybean (NSF 9872565)
Unpublished (1999)
Other_ESTS: AW164281 corresponding to Gm-cl023-42 (5')
Contact: Vodkin, L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)
Lewin, H. A., Director, Keck Center for Comparative and Functional Genomics
University of Illinois
Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Tel: (217) 244-6147
Fax: (217) 333-4582
Email: l-vodkin@uiuc.edu

This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134. For further information call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com
Seq primer: 5'-TTTTTTTTTTTTTTTTT(A/C/G)-3'.

Location/Qualifiers
1. .772

/organism="Glycine max"
/db_xref="taxon:3847"
/clone="Gm-r1070-7633"
/clone.lib="Gm-r1070"
/note="The library Gm-r1070 is a sequence-driven, reracked set of 9,216 clones selected from cDNA libraries from various tissues and stages of development of soybean that represent 2,639 sequences from immature cotyledons, 1,770 from mature seed coats, 3,938 from flowers, and 869 from young pods. The 5' ESTs of the source clones from the different libraries was used to select singletons, or a representative of each contig, which were reracked to form library Gm-r1070. The cDNA clones of the reracked Gm-r1070 library were then sequenced at the 3' end. The contig analysis to select unique genes was performed by the Laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html. Reracking was performed by Genome Systems, St. Louis, http://www.genomesystems.com, and 3' sequencing by the Keck Center for Comparative and Functional Genomics, University of Illinois, http://www.life.uiuc.edu/biotech/keck.html. Note: The corresponding 5' EST from each clone in the Gm-r1070 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Genome Systems clone ID of the original cDNA library that is also listed under 'OTHER EST'."

BASE COUNT 235 a 171 c 113 g 223 t 30 others

ORIGIN

Query Match 7.5%; Score 163.4; DB 10; Length 772;
Best Local Similarity 52.7%; Pred. No. 1.8e-35;
Matches 326; Conservative 0; Mismatches 293; Indels 0; Gaps 0;

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Db 764 GAGTATNCCAAAGGCAACANNNNNNNCAATACNNNNNACATAGGCTNNA 705

QY 1405 actacggagctcaaatgggtgcataacacatgcaggggtatgttaagagcttggcagg 1464

Db 704 CGTATGAGCTAGATGGTGGTTCATATGACATGCGAGGGGTATGCAATACCTTGGTACA 645

QY 1465 catttggaagttcaagggaatggggatgtgggtatgttttgagccacagtagtctgt 1524

Db 644 TGCAAGGATCTTTAGACCAATGCGGTATGTTGAAAAANNCTGAATTCCTTA 585

QY 1525 tggaaaaactgctcttctggtgtgctttcaaccacacatcccccgaacacacccctaa 1584

Db 584 TTGAGAAAGGTCACATAATGAGGTTTTTCTGATCCTAGAAGAACATTTGCTGTGAAGAAAA 525

QY 1585 ttctcaagattaaagtattgactactccttggatgggacaaagccctttcccaacgcccatt 1644

Db 524 CATTAAAGGTAAGAGTCTATATGGGACTGGTTGGAGCTTAGATTTTCAGCCAAACAGACT 465

QY 1645 ttgacctattctacccctccagatttctcactaggtgtgattgtggtggagtgctgctg 1704

Db 464 TTGATACTTACTCGCCACCAAGATTTTATGTTAAAGTTTGTATTTGGAGTTTCTCTGCTG 405

QY 1705 acgagggcaagtggagaacatctgtggtggacaattcatggcaccaccttgaatgagg 1764

Db 404 ATATGGCCAGAGAGAAACAACTGAATTTCAATAAATGCTTTCCTGTTGGATGAAG 345

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Db 344 AGTTTGAATTTCCCTTTGACTGTTCAGAACTGGCTTTCCTCCCATAGAAAGTTTCGAGAGA 285

QY 1825 atgatgatgatgacaaagatgagttgaaggcagacatgccttccatccatgaagtc 1884

Db 284 ATGATAAGAGTCAGAAAGTACTTTTGTGGACAGACATGTTTGTCTGCTCAGAGCTAA 225

QY 1885 gggatgggtatcggtgatgacaaatgtacgacaaagagggcgaatgtactgaaagcgtgc 1944

Db 224 AATCTGGATTCGGATGATGCTCCCTCTCCATGATGAAAGGGTGACAAATTAATAATCTGTGA 165

QY 1945 tgatgtgtttcattttca 1963

Db 164 AGCTTTTGTGCTGTTTCA 146

RESULT 12

AI938235

LOCUS

DEFINITION

sc41e02.yl Gm-cl014 Glycine max cDNA clone EST 30-NOV-2001

Gm-cl014-1683 5' similar to TR:043439 043439

PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C. ; mRNA sequence.

AI938235

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE

AUTHORS

Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Public Soybean EST Project

Unpublished (1999)

Other_ESTS: sc41e02.xl

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Possible reversed clone: similarity on wrong strand This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800) 533-4363 or contact via email: ccu@resgen.com

Seq primer: -40RP from Gibco

732	QY	agcaattacagggccatgctgcagagatttagagcaaatctctcgagacgcctctgat	791
310	Db	CCTGATCTTCAAGCTAAAGTGGCCGAGATGATCACTCAACATTTTGGAGACATCTTG---	366
792	QY	tatccaccacaaactgatcatagtgaggttctctaccggagtcactggaagggaag	851
367	Db	TTCACTCCGGACCARAGTGTTTAAAGAGGTTCCGCTCTCCGAGTCATTTGAANAAACGG	426
852	QY	atcataatctccacaaacccgcgaagtgatctcgaagc	892
427	Db	ATTATATATCACTAAACCAACCCGGAAGGATACCTTTGAAGC	467

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LOCUS	FF637852
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
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ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

RESULT 15
BF637852
LOCUS
DEFINITION
655 bp mRNA linear EST 19-DEC-2000
Phosphate starved leaf Medicago truncatula CDNA
3' end: NF043H05P1. 5' mRNA sequence.

ACCESSION
BF637852
VERSION
BF637852.1
KEYWORDS
EST.
GI:11902010
Medic

SOURCE	ORGANISM
Barber meduc.	<i>Medicago truncatula</i>
	Streptophyta; Embryophyta; Tracheophyta;
	Eukaryota; Viridiplantae;
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
	Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
	<i>Medicago</i> .

REFERENCE AUTHORS	TITLE
1. (bases 1 to 655) Liu, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores H.R., Inman, J.T., Weller, J.W., May, G.D. and Harrison, M.J.	Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula phosphate-starved leaf library Submitted (2000)

Unpublished (2000), NJ
Contact: Harrison Division
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Tel: 580 221 7380
Fax: 580 221 7380
Email: mjharrison@noble.org
Insert length: 655 Std Error: 0.00
Insert depth: 05
Plate: 043 Tow: H Column: 05
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FEATURES source

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seq primer: 1. 635
Location/Qualifiers
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            /clone="NF043H05Pr"
            /clone_lib="Phosphate starved leaf"
            /clone_host="pUC19"
            /clone_vector="pUC19"
            /clone_host="pUC19"
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/tissue-type="trifoliolate"
 /dev-stage="trifoliolate"

/note="vector: lambda zap: At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20uM potassium phosphate. RNA was prepared from above ground tissues."

BASE COUNT	189 a	116 C	145 g	202 c
ORIGIN				

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Best Local Similarity	53.4%	Pred. No. 7.3e-33;		
Matches 321; Conservative	0;	Mismatches 280;	Indels 0;	Gaps 0;

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[illegible]

Db
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[illegible][illegible]

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Oy			
Ddb			
	551	GGCGGCGAGACGTGCCTCCGGTGATGGAGCTGAAGCANGGGATCCGCCGCGTCCCCCTC	610
Oy			
Ddb			
	1911	tacqacaaagaaggcaatgtactgaagcgctgctgattgttttcattt	1960
Oy			
Ddb			
	611	CATGACCAGGCAAGGCAACAGGTACAAGTCCTCAAGCTTCTCATTTGGCTT	660
Oy			
Ddb			

RESULT 14

[illegible]

phosphoinositide-specific phospholipase C, mammalian sequence

leafy spurge.
Euphorbia esula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosales; Rosaceae; Euphorbia.

REFERENCE
1 (bases 1 to 527)
Anderson, J. V. and Horvath, D. P.
AUTHORS
Identification of mRNAs expressed in underground adventitious buds
TITLE
of *Euphorbia esula* (leafy spurge)

**JOURNAL
COMMENT**

Unpublished (2000)
 Contact: Anderson JV
 Plants Science Research
 USDA/ARS, Biosciences Research Lab
 Building 60, Box 5674, Fargo, ND 58105, USA

1605 Aldrecht Blvd., PO Box 50747, Las Vegas, NV 89155-0747
Tel: 701 239 1263
Fax: 701 239 1252
Email: andersjvfargo.ars.usda.gov
Sec printer: pAD5.

FEATURES

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/developmental_stage="3-day induced (decapitated)"	
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		1. Mismatches 171;	Indels 6;	Gaps 2

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QY 495 accggaaccagcttagcagcgacagcagcacccatgcgtcggcactcgggc 554
||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 70 ACCGGGAATCACTTAGTGTAGTTGATTGTAGGATGTCGCCATCGACAGCATTAACAAA 129

QY 555 ggcgtgcgggtgtggaattggaacttgacctga---tgacaaaggcgccatgaagtc 611

Db 130 GGTGTTCGAGTAATCGAATTGGATTTGGCCTAATTCCTTAAGGATAATCTGGATGTT 189

Qy
612 acacacggaacacacattaccaatccgggtgcgttccaaaagtgctgacacagcaccacaa 071

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190 CTTTCATGGAAGGCATTACCAAGTCCCGGAATCATCAAAATGTTGAGCTATCAAG 249

731

[illegible]

1

us-09-828-447-7.rst

Sun Jul 28 10:34:40 2002

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246	QY	ACATGGGAGAGGATGTATTATGATTTCAACATACACATTTTGATGATCTCACCTC	1722
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1663	QY	cagattcttcactagggtgatgtgtgtggagtcctgcgcagcagggcccaagtgaaga	365
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306	QY	CAGACTTCTATGCAAGGGTTGGAATCGCTGGATCCCTTTTGACACTGTTATGAAANAAA	1782
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1723	QY	catctgtgtggaacaattcatgggcaccccatggaaatgagaccatgattgttgcctaa	425
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366	QY	CAAGTCAATANAGATAGTTGGTTGCCCTTCCTGGATGAGGTATTGTGAATTCGCGCTTT	1842
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1783	QY	aatgcccctgaagctcgacactcttcgcatacgaggtccgagaccatgatgatagcaag	485
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426	QY	CGGTTCCGGAGCTGGCACTGCTTCGCATAGAAGTTCATGATATGACATCTCTGAGAGG	1902
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486	QY	ATGATTTTGTGGCAACACATTCCTTCGCTGTGTGGGAATTAAGAAGCGGAATTCGAGCAA	1962
486	Db	ATGATTTTGTGGCAACACATTCCTTCGCTGTGTGGGAATTAAGAAGCGGAATTCGAGCAA	1962
1903	QY	tgaataatgacgacaagaaggcaatgactgaagcgctgatgtgttttcattttc	605
1903	Db	tgaataatgacgacaagaaggcaatgactgaagcgctgatgtgttttcattttc	605
546	QY	TTCCATTACATTCGCCGAAGGANATTAATACAACAATGTAAGCTTCTATGCCCTTTG	605
546	Db	TTCCATTACATTCGCCGAAGGANATTAATACAACAATGTAAGCTTCTATGCCCTTTG	605
1963	QY	a 1963	
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606	QY	a 606	
606	Db	a 606	

search completed: July 26, 2002, 14:51:57
Job time: 6241 sec

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Sequence 3, Appl
Sequence 26, Appl
Sequence 1, Appl
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Sequence 28, Appl
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sequence 225, App
Sequence 2, Appl
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Sequence 17, Appl
Sequence 17, Appl
Sequence 663, App
Sequence 14, Appl
Sequence 1, Appl
Sequence 1, Appl

ALIGNMENTS

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1
RESULT 1
US-08-138-641-1
; Sequence 1, Application US/08138641
; Patent No. 5474921
; GENERAL INFORMATION:
; APPLICANT: Koblan, Kenneth S.
; APPLICANT: Compilano, David L.
; TITLE OF INVENTION: ASSAY TO DETERMINE INHIBITORS OF
; TITLE OF INVENTION: PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C-GAMMA
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Muthard
; STREET: P.O. Box 2000, 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; CURRENT APPLICATION NUMBER: US/08/138.641

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APPLICATION NO: 08-09-138-641-1
FILING DATE: 435
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 18937
TELEPHONE: (908) 594-3903
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3870 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA

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Query Match          4.6%; Score 97.6; DB 1; Length 3870;
Best Local Similarity 51.9%; pred. No. 3.5e+20;
Matches 220; Conservative 0; Mismatches 204; Indels 0; Gaps 0;

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 959 AACCATGACACACCCTGTCTACTATTGGATCTTCTCGCATAATACGTATCTGA 1018

959 AAACCATGAACAACCCACTGTCTCACTATTGGATCCTAAGGCGT

GenCore version 4.5
© 2000 CompuGen Ltd.

1.4 search using sw model

Run on: July 26, 2002, 14:05:57 ; Search time 68.43 Seconds
(without alignments)
7678.066 Million cell updates/sec

US-09-828-447-7

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Sequence:

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 383533 seqs, 122816752 residues 767066

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0
Minimum DB seq length: 2000000000
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Maximum DV seq

post-processing: Minimum Match 0%

Maximum Match 100%
Maximum first 45 summaries
Maximum first 45 summaries

Database :

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, $\frac{b}{c}$ is the number of results predicted by chance to have a score greater than or equal to the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
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2	97.6	4.6	3870	1	US-08-138-133-1	Sequence 1, Appli
3	97.6	4.6	3893	1	US-08-138-641-3	Sequence 3, Appli
4	97.6	4.6	3893	1	US-08-138-133-3	Sequence 3, Appli
5	56.4	2.6	434	4	US-09-118-442-27	Sequence 27, Appli
6	56.4	2.6	434	4	US-09-118-442-27	Sequence 27, Appli
7	53	2.5	7218	1	US-08-232-463-14	Sequence 14, Appli
8	42.2	2.0	11717	1	US-08-801-263A-4	Sequence 4, Appli
9	42.2	2.0	11717	3	US-09-102-248-4	Sequence 4, Appli
10	40.6	1.9	11663	1	US-08-446-932-1	Sequence 1, Appli
11	40.6	1.9	11663	1	US-08-801-263A-1	Sequence 1, Appli
12	40.6	1.9	11663	1	US-08-801-263A-7	Sequence 7, Appli
13	40.6	1.9	11663	3	US-09-102-248-1	Sequence 1, Appli
14	40.6	1.8	11703	1	US-08-801-263A-8	Sequence 8, Appli
15	39.2	1.8	11703	3	US-09-102-248-8	Sequence 8, Appli
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18	39.2	1.8	16656	2	US-08-739-158-1	Sequence 1, Appli
19	39.2	1.8	16656	2	US-08-739-167-1	Sequence 1, Appli
20	39.2	1.8	16656	3	US-08-404-796-1	Sequence 1, Appli
21	39.2	1.8	16656	3	US-08-931-869-1	Sequence 1, Appli
22	39.2	1.8	16656	4	US-09-350-399-1	Sequence 1, Appli
23	39.2	1.7	752	6	5455030-12	Patent No. 5455030
24	35.6	1.7	8298	5	PCT-US93-03076-1	Sequence 1, Appli
25	35.6	1.7	8298	4	US-09-009-443-16	Sequence 16, Appli
26	34.4	1.6	1139	4	US-08-933-750C-60	Sequence 60, Appli
27	34.4	1.6	1460	2		


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; EARLIER FILING DATE: 1997-08-08
; EARLIER APPLICATION NUMBER: 60/053,944
; EARLIER FILING DATE: 1997-07-28
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 434
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(434)
; OTHER INFORMATION: n = A,T,C or G
US-09-118-442-27

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Db 165	tactaggggtaggatctgcagggtgtgaaggcagacagtgatgaagaagacacagggtgat	224		
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1  RESULT      6
2  US-09-677-064-27
3  US-09-677-064-27, Application US/09677064
4  Patent No. 6291224
5  GENERAL INFORMATION:
6  APPLICANT: Martino-Catt, Susan J.
7  APPLICANT: Wang, Hongyu
8  APPLICANT: Beach, Larry R.
9  TITLE OF INVENTION: Genes Controlling Phy
10 TITLE OF INVENTION: Plants and Uses There
11 FILE REFERENCE: 0706D
12 CURRENT APPLICATION NUMBER: US/09/677,064
13 CURRENT FILING DATE: 2000-09-29
14 PRIOR APPLICATION NUMBER: 60/055,446
15 PRIOR FILING DATE: 1997-08-11
16 PRIOR APPLICATION NUMBER: 60/055,526
17 PRIOR FILING DATE: 1997-08-08
18 PRIOR APPLICATION NUMBER: 60/053,944
19 PRIOR FILING DATE: 1997-07-28
20 PRIOR APPLICATION NUMBER: 09/118,442
21 PRIOR FILING DATE: 1998-07-17
22 NUMBER OF SEQ ID NOS: 31
23 SOFTWARE: FastSeq for Windows Version 3.0
24 SEQ ID NO 27
25 LENGTH: 434
26 TYPE: DNA
27 ORGANISM: Zea mays
28 FEATURE:
29 NAME/KEY: misc_feature
30 LOCATION: (1)..(434)
31 OTHER INFORMATION: n = A,T,C or G
32 US-09-677-064-27

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Query Match 2.6%; Score 56.4; DB 4; Length 434;
 Best Local Similarity 57.0%; Pred. No. 7.7e-08;
 Matches 102; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

Qy 1613 gggatgggacaaggccttttccaaagcgcatttgacctattcttcacctccagattttc 1672

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Qy     1673   cactaggtagtatgttgtgggaagcgctgtacacgaggccaagt  
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Db     165   tactagggtaggatcgcatgttggaagcacagacctgtgatga  
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         || | | | | | | | | | | | | | |  
Db     225   tgaggaccagtggtgccgatgtgggatgaggagttcacgtccc  
  
RESULT       7  
US-08-232-463-14/C  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; PRIORITY APPLICATION NUMBER: US/07/935,313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU.  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: ptrzpt-fls  
; JS-08-232-463-14
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us-09-828-447-7.rni

Sun Jul 28 10:34:38 2002

QY 133 tagcatgtgtcgaagtgaagcccaagggatccgagcaagacctgtgtggggagg 192
Db 1201 RRR 1142
QY 193 tgttcaataacagcagagagatgagtgagtgaggggtgtgtgaaattcttgc 252
Db 1141 RRR 1082
QY 253 atacagagcaagggatgtcgacttacccttgatgacgccaagc 297
Db 1081 RRR 1037

RESULT 8
US-08-801-263A-4
; Sequence 4, Application US/08801263A
; Patent No. 5811407
; GENERAL INFORMATION:
; APPLICANT: Johnston, Robert E.
; APPLICANT: Davis, Nancy L.
; APPLICANT: Simpson, Dennis A.
; TITLE OF INVENTION: System for the In Vivo Delivery and
; TITLE OF INVENTION: Expression of Heterologous Genes in the Bone Marrow
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell Seltzer Park & Gibson, P.A.
; STREET: 1211 East Morehead Street
; CITY: Charlotte
; STATE: No. 5811407th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,263A
; FILING DATE: 19-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1171 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-801-263A-4

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Best Local Similarity 54.1%; Pred. No. 0.019;
Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 826 cttcaccggagtcactgaagagagatcataatctccacaaacccgcaagagatc 885
Db 1438 CTTTGCCCATGCTGCTGAGCGAGAGATAAATTTGGCATTACAAACCAAGAGGAGAA 1497
QY 886 tcgaagcatgttccacgcagagaattggccatgagacaggaatctgtgtgagagcttg 945
Db 1498 AACTGCTGCAAGTCCCGAGGAGAAATTAGTCATCGAGGCCAAGGCTCTTTCGAGGATGCTC 1557
QY 946 agaaggaagacaaattggagcagacacacattcgctccc 984
Db 1558 AGGAGGATCCAGAGCGGAGAGAGCTCCGAGAGCACTCC 1596

RESULT 10
US-08-446-932-1
; Sequence 1, Application US/08446932
; Patent No. 5639650
; GENERAL INFORMATION:
; APPLICANT: Johnston, Robert E.
; APPLICANT: Simpson, Dennis
; APPLICANT: Davis, Nancy L.

RESULT 9
US-09-102-248-4
; Sequence 4, Application US/09102248
; Patent No. 6008035
; GENERAL INFORMATION:
; APPLICANT: Johnston, Robert E.
; APPLICANT: Davis, Nancy L.
; APPLICANT: Simpson, Dennis A.
; TITLE OF INVENTION: System for the In Vivo Delivery and
; TITLE OF INVENTION: Expression of Heterologous Genes in the Bone Marrow
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell Seltzer Park & Gibson, P.A.
; STREET: 1211 East Morehead Street
; CITY: Charlotte
; STATE: No. 6008035th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,248
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US 08/801,263
; FILING DATE: 19-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1171 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-102-248-4

Query Match 2.0%; Score 42.2; DB 3; Length 1171;
Best Local Similarity 54.1%; Pred. No. 0.019;
Matches 86; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 826 cttcaccggagtcactgaagagagatcataatctccacaaacccgcaagagatc 885
Db 1438 CTTTGCCCATGCTGCTGAGCGAGAGATAAATTTGGCATTACAAACCAAGAGGAGAA 1497
QY 886 tcgaagcatgttccacgcagagaattggccatgagacaggaatctgtgtgagagcttg 945
Db 1498 AACTGCTGCAAGTCCCGAGGAGAAATTAGTCATCGAGGCCAAGGCTCTTTCGAGGATGCTC 1557
QY 946 agaaggaagacaaattggagcagacacacattcgctccc 984
Db 1558 AGGAGGATCCAGAGCGGAGAGAGCTCCGAGAGCACTCC 1596

RESULT 10
US-08-446-932-1
; Sequence 1, Application US/08446932
; Patent No. 5639650
; GENERAL INFORMATION:
; APPLICANT: Johnston, Robert E.
; APPLICANT: Simpson, Dennis
; APPLICANT: Davis, Nancy L.

```

; TITLE OF INVENTION:  CDNA Clone for South African
; NUMBER OF SEQUENCES:  1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Kenneth D. Sibley
; STREET:  Post Office Drawer 34009
; CITY:  Charlotte
; STATE:  NC
; COUNTRY:  USA
; ZIP:  28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/08/446,932
; FILING DATE:
; CLASSIFICATION:  435
; ATTORNEY/AGENT INFORMATION:
; NAME:  Sibley, Kenneth D.
; REGISTRATION NUMBER:  31,665
; REFERENCE/DOCKET NUMBER:  5470-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  (919) 881-3140
; TELEFAX:  (919) 881-3175
; TELEX:  575102
; INFORMATION FOR SEQ ID NO:  1:
; SEQUENCE CHARACTERISTICS:
; LENGTH:  11663 base pairs
; TYPE:  nucleic acid
; STRANDEDNESS:  single
; TOPOLOGY:  linear
; MOLECULE TYPE:  CDNA
; HYPOTHETICAL:  NO
; US-08-446-932-1

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Query Match      1.9%; Score 40.6; DB 1; Length 11663;
Best Local Similarity 53.5%; Pred. No. 0.061;
Matches 85; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

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QY  886  tcgaagcatgttccacgcagaattggccatggagacaggaatctggtggagagcttg 945
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  1498  AACTGCTGCAAGTCCCGGAGGAATTAGTTATGGAGGCCAAGGCTGTTTCGAGGATGCTC 1557
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  946  agaaggaagacaaattggagcagacacattcgtctccc 984
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RESULT 11
US-08-801-263A-1
; Sequence 1, Application US/08801263A
; Patent No. 5811407
; GENERAL INFORMATION:
; APPLICANT:  Johnston, Robert E.
; APPLICANT:  Davis, Nancy L.
; APPLICANT:  Simpson, Dennis A.
; TITLE OF INVENTION:  System for the In Vivo Delivery and
; NUMBER OF SEQUENCES:  12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Bell Seltzer Park & Gibson, P.A.
; STREET:  1211 East Morehead Street
; CITY:  Charlotte
; STATE:  No. 5811407th Carolina
; COUNTRY:  USA
; ZIP:  28234

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; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/08/801,263A
; FILING DATE:  19-FEB-1997
; CLASSIFICATION:  514
; ATTORNEY/AGENT INFORMATION:
; NAME:  Sibley, Kenneth D.
; REGISTRATION NUMBER:  31,665
; REFERENCE/DOCKET NUMBER:  5470-147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  919-420-2200
; TELEFAX:  919-881-3175
; INFORMATION FOR SEQ ID NO:  1:
; SEQUENCE CHARACTERISTICS:
; LENGTH:  11663 base pairs
; TYPE:  nucleic acid
; STRANDEDNESS:  double
; TOPOLOGY:  linear
; MOLECULE TYPE:  CDNA
; FEATURE:
; NAME/KEY:  CDS
; LOCATION:  60..7559
; FEATURE:
; NAME/KEY:  CDS
; LOCATION:  7608..11342
; US-08-801-263A-1

Query Match      1.9%; Score 40.6; DB 1; Length 11663;
Best Local Similarity 53.5%; Pred. No. 0.061;
Matches 85; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

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QY  886  tcgaagcatgttccacgcagaattggccatggagacaggaatctggtggagagcttg 945
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Db  1558  AGGAGGAATCCAGAGCGGAGAACTCCGAGAGCACTCC 1596
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RESULT 12
US-08-801-263A-7
; Sequence 7, Application US/08801263A
; Patent No. 5811407
; GENERAL INFORMATION:
; APPLICANT:  Johnston, Robert E.
; APPLICANT:  Davis, Nancy L.
; APPLICANT:  Simpson, Dennis A.
; TITLE OF INVENTION:  System for the In Vivo Delivery and
; NUMBER OF SEQUENCES:  12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Bell Seltzer Park & Gibson, P.A.
; STREET:  1211 East Morehead Street
; CITY:  Charlotte
; STATE:  No. 5811407th Carolina
; COUNTRY:  USA
; ZIP:  28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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RESULT 13
US-09-102-248-1
; Sequence 1, Application US/09102248
; Patent No. 6008035
; GENERAL INFORMATION:
; APPLICANT: Johnston, Robert E.
; APPLICANT: Davis, Nancy L.
; APPLICANT: Simpson, Dennis A.
; TITLE OF INVENTION: System for the In Vivo Delivery and
; TITLE OF INVENTION: Expression of Heterologous Genes in the Bone Marrow
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell Seltzer Park & Gibson, P.A.
; STREET: 1211 East Morehead Street
; CITY: Charlotte
; STATE: NC. 6008035th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,248
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/801,263
; FILING DATE: 19-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200

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RESULT 14
US-09-102-248-7
; Sequence 7, Application US/09102248
; Patent No. 6008035
; GENERAL INFORMATION:
; APPLICANT: Johnston, Robert E.
; APPLICANT: Davis, Nancy L.
; APPLICANT: Simpson, Dennis A.
; TITLE OF INVENTION: System for the In Vivo Delivery and
; TITLE OF INVENTION: Expression of Heterologous Genes in the Bone Marrow
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell Seltzer Park & Gibson, P.A.
; STREET: 1211 East Morehead Street
; CITY: Charlotte
; STATE: No. 6008035th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,248
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/801,263
; FILING DATE: 19-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:

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GenCore version 4.5
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Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	546.2	25.5	706	24	AAS17961 P. patens SRSR pr
4	422	19.7	760	21	AAS17960 P. patens SRSR pr
5	161.4	7.5	1066	21	AAC4073 Arabidopsis thalia
6	161.4	7.5	1586	17	AT29716 Phosphatidylinosit
7	97.6	4.6	3870	17	AT12292 Phospholipase C-ga
8	97.6	4.6	3893	17	AT12293 Phospholipase C-ga
9	78.4	3.7	5751	23	ABL07327 Drosophila melanog

10	76.2	3.6	4082	21	AAC76412 Human OREX ORF1967
11	76.2	3.6	10172	22	AAD21290 Human phospholipase
12	76	3.6	1840	22	AAD19219 Human CGI21 (or C5
13	76	3.6	2289	22	AAD17564 Novel human phosph
14	76	3.6	2709	22	AAD17567 Novel human phosph
15	76	3.6	3263	22	AAD16211 Human cDNA sequenc
16	75.4	3.5	5551	23	AAS77856 DNA encoding novel
17	74.4	3.5	2289	24	AAD23721 Human phospholipase
18	74.4	3.5	2462	24	AAD23723 Human phospholipase
19	74.4	3.5	2540	24	AAD23722 Human phospholipase
20	73	3.4	863	22	AAD70553 Human cDNA clone (
21	73	3.4	2416	22	AAL16555 Human cDNA sequenc
22	69.2	3.2	7865	23	ABL07326 Drosophila melanog
23	65	3.0	3425	22	AAL04371 Human phospholipase
24	65	3.0	3544	22	AAL42603 Nucleotide sequenc
25	58.4	2.7	5370	23	ABL07877 Drosophila melanog
26	58	2.7	839	22	AAS40808 Human encoding nove
27	58	2.7	839	22	AAL01837 Human reproductive
28	57.2	2.7	4907	23	ABL06441 Drosophila melanog
29	53	2.5	5233	17	AAT58225 DNA encoding inosi
30	52.4	2.4	764	22	ABA08435 Human pancreas pho
31	52.4	2.4	911	22	AAS41437 cDNA encoding nove
32	52.4	2.4	2265	24	ABA05630 Human phosphoester
33	52.4	2.4	2288	22	AAS40806 cDNA encoding nove
34	52.4	2.4	2945	22	AAL15778 Human cDNA sequenc
35	52	2.4	37996	23	ABL07876 Drosophila melanog
36	47.6	2.2	406	22	AAL65951 Novel human polynu
37	47.4	2.2	1977	22	AAL17609 Human cDNA sequenc
38	45	2.1	1160	22	AAS40809 cDNA encoding nove
39	43.8	2.0	1490	22	AAD19225 Human CGI21 (or C5
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41	42.2	2.0	11717	19	AAV33474 Girdwood S.A.virus
42	41.2	1.9	6252	22	AAK53310 Human polynucleoti
43	41.2	1.9	6813	22	AAK52326 Human polynucleoti
44	41	1.9	2338	22	AAL16583 Human cDNA sequenc
45	41	1.9	5150	23	AAS76239 DNA encoding novel

ALIGNMENTS

RESULT 1	
AAS17966	
ID AAS17966 standard; cDNA; 2139 BP.	
XX	
AC AAS17966;	
XX	
DT 12-MAR-2002 (first entry)	
XX	
DE P. patens signal transduction stress-related protein PLC-2 cDNA.	
XX	
KW Signal transduction stress-related protein; SRSR; PLC-1; PLC-2;	
KW 14-3-3p-1; 14-3-3p-2; CBP-1; phospholipase C; Ca2+ binding protein;	
KW transgenic plant; environmental stress; salinity; drought;	
KW low temperature; ss.	
XX	
OS Physcomitrella patens.	
XX	
EH Key Location/Qualifiers	
FT CDS 123..2009	
FT /*tag= a	
FT /product= "PLC-2"	
XX	
XX WO200177355-A2.	
XX	
PD 18-OCT-2001.	
XX	
PF 06-APR-2001; 2001WO-US11398.	
XX	
PR 07-APR-2000; 2000US-196001P.	
XX	
PA (BADI) BASF PLANT SCI GMBH.	

PI	Costa Silva EO, Bohnert HJ, Van Thienen N, Chen R, Ishitani M;
XX	
DR	WPI; 2002-049152/06.
DR	P-PSDB; AAU11620.
DR	
PT	New polypeptide, useful for increasing tolerance to environmental
PT	stress, comprises a Signal Transduction Stress-Related Protein selected
PT	from phospholipases, 14-3-3 proteins and calcium binding proteins
XX	
XX	Claim 4; Fig 2B; 101pp; English.
XX	
CC	The invention relates to a Signal Transduction Stress-Related Protein
CC	(STSRP) isolated from Physcomitrella patens, and selected from
CC	Phospholipase C (PLC)-1 protein, PLC-2 protein, 14-3-3 protein
CC	(14-3-3P)-1, 14-3-3P-2 and Ca ²⁺ -Binding Protein (CBP)-1, or their
CC	orthologues. Also include are a transgenic plant transformed with
CC	an STSRP coding nucleic acid, where the expression of the nucleic acid in
CC	the plant cell results in increased tolerance to an environmental stress
CC	as compared to a wild type variety of the plant cell, a nucleic
CC	acid encoding an STSRP, and an expression vector comprising the nucleic
CC	acid. The STSRP and nucleic acids are useful for increasing tolerance to
CC	acid. The STSRP and nucleic acids are useful for increasing tolerance to
CC	environmental stress selected from salinity, drought and low temperature,
CC	in transgenic plants including monocot and dicot selected from maize,
CC	wheat, rye, oat, triticale, rice, barley, soybean, peanut, cotton,
CC	rapiessed, canola, manihot, pepper, sunflower, tagetes, solanaceous
CC	plants, potato, tobacco, eggplant, tomato, Vicia species, pea, alfalfa,
CC	coffee, cacao, tea, Salix species, oil palm, coconut, perennial grass and
CC	forage crops. The nucleic acid is also useful for identifying organisms
CC	e.g. Physcomitrella patens in a mixed population of microorganisms,
CC	for evolutionary and protein structural studies and are useful as markers
CC	for specific regions of the genome. The present sequence encodes PLC-2.
XX	
XX	Sequence 2139 bp: 588 A: 497 C: 564 G: 490 T: 0 other:

	Query Match	100.0%	Score 2139;	DB 24;	Length 2139;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 2139;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	atcccgggcttcggaggtttaagagatgtcacggcgtgggaagacagagcggtgatgca	60		
Db	1	atcccgggcttcggaggtttaagaggaagtacacggcgtgggaagacagagcggtgatgca	60		
Qy	61	ggtttgggtgagcttaaggttgacggagtgtaagggtatcgcttgcactgggtttgca	120		
Db	61	ggtttgggtgagcttaaggttgacggagtgtaagggtatcgcttgcactgggtttgca	120		
Qy	121	aaatgtgttcataagcatgtgtcgaaatgaaacccgaaggggatccgagcaagacc	180		
Db	121	aaatgtgttcataagcatgtgtcgaaatgaaacccgaaggggatccgagcaagacc	180		
Qy	181	tggtggggaggtgttcacaatacacagcgagaatgagagatgagtcgaggggttgc	240		
Db	181	tggtggggaggtgttcacaatacacagcgagaatgagagatgagtcgaggggttgc	240		
Qy	241	tgaattcttgcatacagagaagggtgtgcacttcaccccttgatgagcccaagaga	300		
Db	241	tgaattcttgcatacagagaagggtgtgcacttcaccccttgatgagcccaagaga	300		
Qy	301	tcattgagcgcatccgaagactggaagaatccttcggactcgccctctatcaactcag	360		
Db	301	tcattgagcgcatccgaagactggaagaatccttcggactcgccctctatcaactcag	360		
Qy	361	actgtcgaaggaggtctttcggaaagtacttgatgaatcccgacttgatggcgctttac	420		
Db	361	actgtcgaaggaggtctttcggaaagtacttgatgaatcccgacttgatggcgctttac	420		
Qy	421	acaaagtgtttaccaagacatgacgacgcgatctgcactatttcatttcacgggcc	480		
Db	421	acaaagtgtttaccaagacatgacgacgcgatctgcactatttcatttcacgggcc	480		
Qy	481	ataactcgtacctgaccggcaaccagtgaagcagcgacagcagcagcaccatcgctg	540		

[illegible]

CC acid encoding an STSRP, and an expression vector comprising the nucleic
 CC acid. The STSRP and nucleic acids are useful for increasing tolerance to
 CC environmental stress selected from salinity, drought and low temperature,
 CC in transgenic plants including monocot and dicot selected from maize,
 CC wheat, rye, oat, triticale, rice, barley, soybean, peanut, cotton,
 CC rapeseed, canola, manihot, pepper, sunflower, tagetes, solanaceous
 CC plants, potato, tobacco, eggplant, tomato, Vicia species, pea, alfalfa,
 CC coffee, cacao, tea, Salix species, oil palm, coconut, perennial grass and
 CC forage crops. The nucleic acid is also useful for identifying organisms
 CC e.g. Physcomitrella patens in a mixed population of microorganisms,
 CC for evolutionary and protein structural studies and are useful as markers
 CC for specific regions of the genome. The present sequence is a partial
 CC cDNA for PLC-2.
 XX
 SQ

Sequence 706 BP; 220 A; 181 C; 171 G; 133 T; 1 other;

Query Match 25.5%; Score 546.2; DB 24; Length 706;
 Best Local Similarity 95.9%; Pred. No. 1.1e-161;
 Matches 636; Conservative 0; Mismatches 18; Indels 9; Gaps 7;

QY 596 agcgcatgaaggtcacacacggaacacacattaccatccgggtgtgtccaaaagtg 655

Db 8 agcgcatgaaggtcacacacggaacacacattaccatccgggtgtgtccaaaagtg 67

QY 656 tgcacagccatcaagaataaagccttctccctcgagtagccacagtttgcgttactat 715

Db 68 tgcacagccatcaagaataaagccttctccctcgagtagccacagtttgcgttactat 127

QY 716 tgaggatctttacaagcgaattacagggccatgctgcagagatttagacaaattct 775

Db 128 tgaggatctttacaagcgaattacagggccatgctgcagagatttagacaaattct 187

QY 776 cggagacccctgtattatcccccacacactgattgaggttccctccaccgga 835

Db 188 cggagacccctgtattatcccccacacactgattgaggttccctccaccgga 247

QY 836 gtcactgaagaggaagatcataatctccaccacacccggaagtagtcttcgaagcgtg 895

Db 248 gtcactgaagaggaagatcataatctccaccacacccggaagtagtcttcgaagcgtg 307

QY 896 ttccacgagaattggccatggagaacagggaattctgtggaggagcttgagaagaaga 955

Db 308 ttccacgagaattggccatggagaacagggaattctgtggaggagcttgagaagaaga 367

QY 956 caaattgagacagaccattgctcccttgaaagagaacacacatcctgggagaataac 1015

Db 368 caaattgagacagaccattgctcccttgaaagagaacacacatcctgggagaataac 427

QY 1016 accatgctgcgtgaagtagcaggttttaagcccaaaaggaatgtcaaccacc-agctg 1074

Db 428 accatgctgcgtgaagtagcaggttttaagcccaaaaggaatgtcaaccaccagctg 487

QY 1075 agcttaactctagaa---gtcccttgacctcgggggaagcaa-catccacaaggttatgc 1130

Db 488 agcttaactctagaa---gtcccttgacctcgggggaagcaa-catccacaaggttatgc 547

QY 1131 -aagagcaacgtgcaatgacaacccct-aaacatttcaagtatcccggtctatcaaca 1188

Db 548 aagagcaacgtgcaatgacaacccct-aaacatttcaagtatcccggtctatcaaca 607

QY 1189 tcgggtgaaagcacgcaaaaggggacatcgatgagcagctgactgcaagtcgatgat 1248

Db 608 tcgggtgaaagcacgcaaaaggggacatcg-tggcctgcgactgcagtcgatgat 665

QY 1249 cag 1251

Db 666 cag 668

RESULT 4

ID AAS17960 standard; cDNA; 760 BP.

XX AAS17960;

AC 12-MAR-2002 (first entry)

DE P. patens STSRP protein, PLC-1, partial cDNA.

XX Signal transduction stress-related protein; STSRP; PLC-1; PLC-2;
 XX 14-3-3p-1; 14-3-3p-2; CBP-1; phospholipase C; Ca²⁺ binding protein;
 XX transgenic plant; environmental stress; salinity; drought;
 XX low temperature; ss.

OS Physcomitrella patens.

XX WO200177355-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-US11398.

XX 07-APR-2000; 2000US-196001P.

XX (BADI) BASF PLANT SCI GMBH.

XX Costa Silva EO, Bohnert HJ, Van Thielien N, Chen R, Ishitani M;

XX WPI; 2002-049152/06.

XX New polypeptide, useful for increasing tolerance to environmental
 XX stress, comprises a Signal Transduction Stress-Related protein selected
 XX from phospholipases, 14-3-3 proteins and calcium binding proteins -
 XX Example 5; Fig 1A; 101pp; English.

XX The invention relates to a Signal Transduction Stress-Related Protein
 CC (STSRP) isolated from Physcomitrella patens, and selected from
 CC phospholipase C (PLC)-1 protein, PLC-2 protein, 14-3-3 protein
 CC (14-3-3P)-1, 14-3-3P-2 and Ca²⁺ Binding Protein (CBP)-1, or their
 CC orthologues. Also include are a transgenic plant transformed with
 CC an STSRP coding nucleic acid, where the expression of the nucleic acid in
 CC the plant cell results in increased tolerance to an environmental stress
 CC as compared to a wild type variety of the plant cell, a nucleic
 CC acid encoding an STSRP, and an expression vector comprising the nucleic
 CC acid. The STSRP and nucleic acids are useful for increasing tolerance to
 CC environmental stress selected from salinity, drought and low temperature,
 CC in transgenic plants including monocot and dicot selected from maize,
 CC wheat, rye, oat, triticale, rice, barley, soybean, peanut, cotton,
 CC rapeseed, canola, manihot, pepper, sunflower, tagetes, solanaceous
 CC plants, potato, tobacco, eggplant, tomato, Vicia species, pea, alfalfa,
 CC coffee, cacao, tea, Salix species, oil palm, coconut, perennial grass and
 CC forage crops. The nucleic acid is also useful for identifying organisms
 CC e.g. Physcomitrella patens in a mixed population of microorganisms,
 CC for evolutionary and protein structural studies and are useful as markers
 CC for specific regions of the genome. The present sequence is a partial
 CC cDNA for PLC-1.

XX Sequence 760 BP; 198 A; 178 C; 201 G; 183 T; 0 other;

Query Match 19.7%; Score 422; DB 24; Length 760;
 Best Local Similarity 74.0%; Pred. No. 2e-122;
 Matches 549; Conservative 0; Mismatches 190; Indels 3; Gaps 1;

QY 154 ccccgaaagggatcccgagcaagacctgtgtggggaggttctcaataatacagcaga 213

Db 9 ccaagaaggggtttgctgcagatatttggggaggtgtgtctgactacagcaga 68

QY 214 atgagagtagtgctgcgaggggttctgaaattctgcatacacagagggatgtcg 273

Db 69 atgggaagctggacgcgaggggttctgtaagtcttctgcagacagcaaggggagca 128

QY 274 acttcacccttgatgacgccaagcagatcatggagcgcttcgcaaggagctggaagaaat 333

Db 129 agtcctctctagatgacgcaagcacctagtggagttgattgattggaatgagacataagt 188
QY 334 c---cttcgactcgcctctatacaactcaactgactgtcgaaggagcgttttcgaaagtact 390
Db 189 cgaattccctcgtggttcactcgtcgtcgtgacgtcgtcgaagggtgattttaaactctg 248
QY 391 tgatgaatcccgacttgatggcgtcttacaaacgttcttaccacgaacatgacgcagc 450
Db 249 tactgagccggattgaatgggttcttgaagcaactgtgcatcaagacatgacgcagc 308
QY 451 cgaatgcgaactattcatattcaatgagccatcaactcgtacactgacgcgaacacagctga 510
Db 309 cgttatcgcaacttctcatattcaactggtcacaactcgtacttgacgggtaacacagctta 368
QY 511 qcagcacagcagcagcac 570
Db 369 gcagcgacagtagcgacgttccctatgctgctgcaactgcaacgtggtggtggtggtg 428
QY 571 aattgacttgcctgatgacaaaggcggcgtgacgacacacacacacacacacacacacac 630
Db 429 aactggttgcctgacgataaaggcggcgtgacacacacacacacacacacacacacac 488
QY 631 ccaatccggtggttcacaaaggcggcgtgacacacacacacacacacacacacacacac 690
Db 489 ccagtcaggttgcctgacgataaaggcggcgtgacacacacacacacacacacacacac 548
QY 691 cgaatccggtggttcacaaaggcggcgtgacacacacacacacacacacacacacacac 750
Db 549 cgaatccggtggttcacaaaggcggcgtgacacacacacacacacacacacacacac 608
QY 751 ctgcagagatttagacaaaggcggcgtgacacacacacacacacacacacacacacac 810
Db 609 ctgcagagatttagacaaaggcggcgtgacacacacacacacacacacacacacacac 668
QY 811 cattagtgagttcttcac 870
Db 669 ggtttaaagacgtccttcac 728
QY 871 cgcgcaaggagtagtctcgaagc 892
Db 729 cgcgcaaggagtagtctcgaagc 750

RESULT 5
AAC40773
ID AAC40773 standard; DNA; 1066 BP.
XX AC AAC40773;
XX AC AAC40773;
XX AC AAC40773;
DT 17-OCT-2000 (first entry)
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 29497.
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 29497.
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX Arabidopsis thaliana.
XX Arabidopsis thaliana.
PN EF1033405-A2.
XX EF1033405-A2.
PD 06-SEP-2000.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.

FT			sequence are substd. by CGCGG, both coding
FT			for Arg-Arg, since tandem AGG codons are
FT			associated with poor protein expression
FT			in E. coli"
FT	misc_feature	3871..3893	
FT		/tag= b	
FT		/note= "bases 3871-3893 are added to the 3' end	
FT		of the natural sequence and encode an	
FT		epitope tag"	
XX			
PN	US5474921-A.		
PD			
PD	12-DEC-1995.		
XX			
PF	15-OCT-1993;	93US-0138641.	
XX			
PR	15-OCT-1993;	93US-0138641.	
XX			
PA	(MERI) MERCK & CO INC.		
XX			
PI	Koblan KS, Pompliano DL;		
XX			
DR	WPI; 1996-048545/05.		
XX			
PT	Method for expression and isolation of mammalian phospholipase		
PT	C-gamma-1 - useful for determining inhibitory activity of test		
PT	compounds towards phospho:inositide-specific phospholipase-C enzyme.		
XX			
PS	Example; Column 19-24; 25pp; English.		
XX			
CC	cDNA coding for phosphoinositide-specific phospholipase C-gamma-1		
CC	(AAR0583) was modified by substituting an AGAGG sequence associate		
CC	with poor expression in E. coli and by attachment of DNA coding for		
CC	an epitope tag at the 3' end of the sequence. The resulting cDNA		
CC	(AAT12293) is suitable for expression in transformed bacterial host		
CC	cells with affinity purification of the recombinant PIC-gamma-1.		
XX			
SQ	Sequence 3893 BP; 925 A; 1050 C; 1093 G; 825 T; 0 other;		
Query Match	4.6%; Score 97.6; DB 17; Length 3893;		
Best Local Similarity	51.9%; Pred. No. 1.9e-19;		
Matches 220; Conservative	0; Mismatches 204; Indels	0; Gaps	
QY	436 aaagacatcagcgagccgatgctgcgaatttcataatttcacggcgcatcaactgtacctga	496	
Db			
QY	496 ccggcaaccaggctgagcagcgacgagcgacacaccccatacgtctgcgcactgcgcgcg	555	
Db			
QY	1019 ctggggaccagtctccagcgagctccctcctggaagcctaectgcctgcgtgaggtgg	1077	
Db			
QY	556 gcgtgcgggttgtaattggaattgaccttgcgcctgatgacaaagcgcgcatgaaggtcacac	615	
Db			
QY	1079 gctgctgcgtgcagctgagttggaatgctgggatgggccagatgggatgcagtcatttacc	1133	
Db			
QY	616 acggaacacacacttaccaatccggtgctgtccaagaagtgtcacagccatcaagaata	6797	
Db			
QY	1139 atggggcacacctcaccaagaattaatgtctcagatgctcgcacaccatcagaagc	1191	
Db			
QY	676 acgctctttcaactcggagtagccccagtttgctgtactattgagatcatcttacaagcg	735	
Db			
QY	1199 acgctgtcgtagctcagtagtaccctgtcatcgttccatcagagaccactgcagcattg	1255	
Db			
QY	736 aattacagggccatgctgcagagatttttagacaaattctcggagagccctgtattatc	795	
Db			
QY	1259 cccagcagaggaacatggcccagcacttcaggaaaggtgctcgtgcacgctcctoacca	1311	
Db			
QY	796 caccacaactgatgattagtgaggtttcotctaacccggagtcactgaaggaagatca	855	
Db			
QY	1319 agccctggacattgcgcgtgatggctcccttctctcccaaccagctcaagaggaatcc	1377	
Db			
QY	856 taat	859	

Db	1379	tgat 1382	
Db	1378	catcgagttgattgttggaacggccgcaaatctgcctacatatatttcacggccacac	
Qy	626	acttaccatccgggtgctgttccaaaagtgtgtcacagccatcaagaataacgcttctt	
Db	1438	cattacctcaagatcaagtctatgtgtgtatcagagcagattagagatcatgcttccac	
Qy	686	cacctcgagtagcccaagtttgcgttactattgagagatcatcttacaagcgaattacaggg	
Db	1498	cagttccgagtagcccgtaattattgtccatagacgagaattgctccctggacagcagcg	
Qy	746	ccatgtgtcagagatttttagagcaaatcttcgagagacccctgtattatccaccaccaac	
Db	1558	gaatatggcgagcgttgcgtgaggttttcggggatagctgcttagcgaaccttgtga	
Qy	806	tgatgattagtgaggtttctccacggagtcactcagagagagagatcataatctccac	
Db	1618	tcgaacagcagcagcacttccatccatccaggttgctgcgaagataatctctgaagca	
Qy	866	caaacgccggaagtagtatctega	889
Db	1678	caagaagtgcgcagtttgacga	1701
RESULT	10		
AAC76412			
ID	AAC76412	standard; cDNA; 4082 BP.	
XX			
AC	AAC76412;		
XX			
DT	08-FEB-2001	(first entry)	
XX			
DE	Human ORFX ORF1967	polynucleotide sequence SEQ ID NO:3933.	
XX			
KW	Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;		
KW	vulnary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;		
KW	anticonvulsant; osteopathic; antiarthritis; immunosuppressant; cardiac;		
KW	immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;		
KW	hypotensive; dermatological; immunosuppressive; antiinflammatory;		
KW	antiviral; antibacterial; antifungal; antirheumatic; antithyroid;		
KW	antianemic; gene therapy; cancer; proliferative disorder; hypertension;		
KW	neurodegenerative disorder; osteoarthritis; graft vs host disease;		
KW	cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;		
KW	cholesterol ester storage; systemic lupus erythematosus; infection;		
KW	severe combined immunodeficiency; malaria; autoimmune disorder; asthma;		
KW	allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;		
KW	bone damage; cartilage damage; antiinflammatory disease; coagulation;		
KW	thrombosis; contraceptive; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200058473-A2.		
XX			
PD	05-OCT-2000.		
XX			
PF	31-MAR-2000; 2000WO-US08621.		
XX			
PR	31-MAR-1999; 99US-0127607.		
PR	02-APR-1999; 99US-0127636.		
PR	05-APR-1999; 99US-0127728.		
PR	30-MAR-2000; 2000US-0540763.		
XX			
PA	(CURA-) CURAGEN CORP.		
XX			
PI	Shimkets RA, Leach M;		
XX			
XX	WPI; 2000-602362/57.		
XX	P-PSDB; AAB42203.		
XX	Novel nucleic acids and peptides derived from open reading frame X,		
PT	useful for treating e.g. cancers, proliferative disorders,		
PT	neurodegenerative disorders and cardiovascular disease -		
XX			

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Qy	866	caaacgccggaagtagtatctega	889
Db	1678	caagaagtgcgcagtttgacga	1701
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ID	ABL07327	standard; cDNA; 5751 BP.	
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AC	ABL07327;		
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DT	26-MAR-2002	(first entry)	
XX			
DE	Drosophila melanogaster expressed polynucleotide SEQ ID NO 16463.		
XX			
KW	Drosophila; developmental biology; cell signalling; insecticide;		
KW	pharmaceutical; gene; ss.		
XX			
OS	Drosophila melanogaster.		
XX			
PN	WO200171042-A2.		
XX			
PD	27-SEP-2001.		
XX			
PF	23-MAR-2001; 2001WO-US09231.		
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PR	23-MAR-2000; 2000US-191637P.		
PR	11-JUL-2000; 2000US-0614150.		
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PA	(PEKE) PE CORP NY.		
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PI	Venter JC, Adams M, Li PWD, Myers EW;		
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DR	WPI; 2001-656860/75.		
DR	P-PSDB; ABB63224.		
PT	New isolated nucleic acid detection reagent for detecting 1000 or more		
PT	genes from Drosophila and for elucidating cell signalling and cell-cell		
PT	interactions -		
XX			
PS	Claim 1; SEQ ID NO 16463; 21pp + Sequence Listing; English.		
XX			
CC	The invention relates to an isolated nucleic acid detection reagent		
CC	capable of detecting 1000 or more genes from Drosophila. The invention is		
CC	useful in developmental biology and in elucidating cell signalling and		
CC	cell-cell interactions in higher eukaryotes for the development of		
CC	insecticides, therapeutics and pharmaceutical drugs. The invention		
CC	discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA		
CC	sequences (ABL01840-ABL16175) and the encoded proteins		
CC	(ABB57737-ABB72072).		
CC	The sequence data for this patent did not form part of the printed		
CC	specification, but was obtained in electronic format directly from WIPO		
CC	at ftp.wipo.int/pub/published_pct_sequences.		
XX			
SQ	Sequence 5751 BP; 1605 A; 1257 C; 1329 G; 1560 T; 0 other;		
Query Match	3.7%; Score 78.4; DB 23; Length 5751;		
Best local similarity	47.2%; Pred. NO. 2.9e-13;		
Matches	238; Conservative 0; Mismatches 266; Indels 0; Gaps 0;		
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Qy	446	gcagcggatgctgcactatttcatatttcacggccataactcgtacgtgacggcaacca	505
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Qy	506	gctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	565
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Qy	566	tgtggaattgactgtggcctgtgacaaagcggcagcaggtgacacacagcgaacac	625

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 26, 2002, 13:34:42 ; Search time 3923.35 Seconds
(without alignments)
11409.092 Million cell updates/sec

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Perfect score: 2139

Sequence: 1 atcccggttcgaggttt.....gtgcacccaaggttaacgcc 2139

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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7: gb_ph.*

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11: gb_sts.*

12: gb_sv.*

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14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

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21: em_or.*

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32: em_htg_other.*

33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description

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2	841.6	39.3	2276	6	AX2811100	AX2811100 Sequence
3	546.2	25.5	706	6	AX281096	AX281096 Sequence
4	422	19.7	760	6	AX281095	AX281095 Sequence
5	283.8	13.3	2134	8	GMU41474	U41474 Glycine max
6	280.2	13.1	2079	8	GMU25027	U25027 Glycine max
7	258.4	12.1	2113	8	PSPLC	Y15253 Pisum sativ
8	254	11.9	1776	8	AY053422	AY053422 Arabidops
9	249.4	11.7	2038	8	DSA291467	AJ291467 Digitaria
10	247.6	11.6	1894	8	GMU41473	U41473 Glycine max
11	243.4	11.4	1746	8	AF108123	AF108123 Brassica
12	240.2	11.2	2170	8	GMU41475	U41475 Glycine max
13	233.4	10.9	2207	8	AF332874	AF332874 Oryza sat
14	229.4	10.7	2066	8	NRPHOSIPC	X95877 N.rustica m
15	224.6	10.5	2013	8	NRPHOSIPC	X95877 N.rustica m
16	221.4	10.4	1981	8	STPLCIGEN	Y11931 N.rustica m
17	218.6	10.2	1746	8	AY040054	AY040054 Arabidops
18	218.6	10.2	2032	8	AF360206	AF360206 Arabidops
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20	214.6	10.0	2394	8	AF2233573	AF2233573 Nicotiana
21	212.6	9.9	1940	8	STPLC2	X94183 S.tuberosum
22	207.8	9.7	1985	8	AY062681	AY062681 Arabidops
23	202.2	9.5	2006	8	VU085250	U85250 Vigna ungui
24	195.6	9.1	2009	8	STPLC3	X94289 S.tuberosum
25	181	8.5	2098	8	AF223351	AF223351 Nicotiana
26	161.4	7.5	1686	23	EL1091	EL1091 cDNA coding
27	161.4	7.5	1961	8	ATHATPLC1	D38544 Arabidops
28	153.4	7.2	1841	8	ATU13203	U13203 Arabidops
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30	109.2	5.1	4344	4	BTPLCII	Y00301 Bovine mRNA
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32	98.6	4.6	3201	5	AF090112	AF090112 Xenopus l
33	98.4	4.6	2791	10	RATPLC3A	M20637 Rat phospho
34	98.2	4.6	530	8	AF434168	AF434168 Arabidops
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36	97.6	4.6	3870	6	II1308	II1308 Sequence 1
37	97.6	4.6	3893	6	II16138	II16138 Sequence 1
38	97.6	4.6	3893	6	II1309	II1309 Sequence 3
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42	94	4.4	4242	9	HSPLC	X14034 Human mRNA
43	94	4.4	4242	9	HUMPLC	M37238 Human phosph
44	93.8	4.4	560	8	AF434167	AF434167 Arabidops
45	93.8	4.4	2660	10	AF133125	AF133125 Mus muscu

ALIGNMENTS

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LOCUS	AX2811101	Sequence 7 from Patent WO0177355.				
DEFINITION	AX2811101	Sequence 7 from Patent WO0177355.				
ACCESSION	AX2811101	Sequence 7 from Patent WO0177355.				
VERSION	AX2811101.1	GI:16608368				
KEYWORDS		Phycomitrella patens.				
SOURCE		Phycomitrella patens.				
ORGANISM		Phycomitrella patens.				

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

588 a

437 c

564 g

490 t

QY 2101 agactgaccagtttagtctgaccccaaggttaacgcc 2139
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Db 2101 AGACTGACCAGTTAGTGTGTCACCCCAAGGTTAACGCC 2139

RESULT 2
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LOCUS AX281100 2276 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 6 from Patent WO0177355.
ACCESSION AX281100
VERSION AX281100.1 GI:16608367
KEYWORDS
SOURCE Physcomitrella patens.
ORGANISM Physcomitrella patens.
Eukaryota; Viridiplantae; Streptophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
1 (sites)
costa e Silva, O.D., Bohnert, H.J., van Thielens, N., Chen, R. and
Ishitani, M.
TITLE Signal transduction stress-related proteins and methods of use in
Plants
JOURNAL Patent: WO 0177355-A 6 18-OCT-2001;
BASF Plant Science GmbH (DE)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:3218"
BASE COUNT 626 a 481 c 609 g 560 t
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Query Match 39.3%; Score 841.6; DB 6; Length 2276;
Best Local Similarity 67.7%; Pred. No. 4.8e-246;
Matches 1304; Conservative 0; Mismatches 524; Indels 98; Gaps 5;

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Db 173 GGTGTCGAGGGATTTATTTGTGCGGTAGCTGGGTTTGC AAAATGTGTTCTATTCCGTT 232
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QY 140 ttgtcgaagtggaaaccccgagggagtcgagcagcaaacctgtgtggagaggtttcac 199
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QY 200 aatatacagcagagatgagagatgagtcgaggggtgtgtaaatcttgcatacaga 259
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Db 293 GACTTACAGCAGAGATGGGAAGCTGAGCGCCGAGGGTTGCTGAAGTTCTTGGCAGACA 352
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Db 413 TGAGAGACATAAGTCGAATATCCCTGGGTTTCATGCTCAGCTCGACCTGTGCGAGGGTGA 472
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QY 377 ttctcgaagtacttgatgaatcccgacttgaaatggcgtcttcaacaacgtgttcacca 436
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Db 473 TTTTAAAACTATGACTGAGCCCGGATTTGAATGGGGTTCTTGAAGACACTGTGTCATCA 532
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QY 437 agacatgacgacgcagtcgtcgactatttcatattcattcagcgcccaataactcgtacctgac 496
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Db 533 AGACATGACGACGCGTTATCGCACTACTTCAATTTACTGCTGGTTCACAACTTCGTACTTGAC 592
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QY 497 cggcaaccagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 556
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Db 593 GGGTAACCAAGCTTACACGACAGATAGCGACGTTCCCATTTGCTGCTCACTGCAACAGTGG 652
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QY 557 cgtgcgggtgttgaaattggactgtgacctgatgacaaaggcggatgaaggtcacaca 616
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QY 617 cggaaacacacttaccatccggtgtgtgttccaaagtggtcacagccatcaagaataa 676
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QY 917 ggagaaacaggaattctgtggagagcttgagaaggaagacaaattggagcagaccacatt 976
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QY 977 cgtccctctgaa-----gagaaacacatcctcgtggagaaaaa 1014
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QY 1121 aaggtatagcaagagcaacgtaggcaatgacacacccctaaacatttcaagtagtgcggct 1180
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Db 1253 AGCGGATGTGAAGATGACGATG---ACGACANTAAAGAAATCCTGAGTATGCTCGGCT 1309
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QY 1181 catcaaatccggctgtagcaaacgacgcaaggggagacatcgatggagcatcgactgcaagt 1240
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Db 1370 TGAAGGACAGTGTGACGGATTAGTCTTTCAGAGACTAAGCTGGAGAAAGTCACTGAAGA 1429
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QY 1301 gtggcccggaagctctgtgtaaatccacgacagaaacatttacctgtgtatcctgctgc 1360
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Db 1430 GTTCTCTGAACCTGTGGTCAAGTTCCAGGATTCATGATCTCTGCGCTTGGATTCACGAGTCAAT 1549
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1841 agatgagttgaaggagacacatctccatccatccatgaagtccgagtggtatcggtg 1900
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1974 GTGCGATGATGACAAAGGCGAGTGTGTTGAAGGGCGTGAAATGTTGTTCATTT 2033
1961 tcaaaa 1966
2034 TCAAAA 2039

RESULT 3
AX281096 AX281096 706 bp DNA linear PAT 02-NOV-2001
LOCUS
DEFINITION Sequence 2 from Patent WO0177355.
ACCESSION AX281096
VERSION AX281096.1 GI:16608363
KEYWORDS
SOURCE Physcomitrella patens.
ORGANISM Physcomitrella patens.
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
AUTHORS Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
1 (sites)
TITLE costa e Silva, O.D., Bohnert, H.J., van Thiel, N., Chen, R. and
Ishitani, M.
JOURNAL Signal transduction stress-related proteins and methods of use in
plants
PATENT: WO 0177355-A 2 18-OCT-2001;
BASF Plant Science GmbH (DE)
FEATURES
Location/Qualifiers
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/db_xref="taxon:3218"
BASE COUNT 220 a 181 c 171 g 133 t 1 others
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Best Local Similarity 95.9%; Pred. No. 1.3e-155;
Matches 636; Conservative 0; Mismatches 18; Indels 9; Gaps 7;

596 agcgccatgaaggtcacacacggaacacacttaccatccggtgcttccaaaagt 655
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836 gtcaactgaaggaagatcatataatctccacaaacccggaaggaggtatctcgaagatg 895
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428 ACCATCTCTGCTTGAAGAGTTCGAGGTTTAAAGCCAAAAGGAAATGTCAACCAAGCTG 487
1075 agcttaactctagaa---gtccctctgacccctcggggaagcaaa-catacaaaaggtatagc 1130
488 AGCTTAACCTCTAGAAAGTCTCTCTGACCTCGGGGAAGCAACCATCCAAAGGTATAGC 547
1131 -aaagacaagatgagcaatcaaacacct-aaacatttcaagtatgcccggctcatcaaaa 1188
548 AAAGAGCAACGATGGCAATGACAAACCTTAAACATTTCAAGTATGCCCGGTTTCATCAACA 607
1189 tccggctagcaagcagcaaggggacatcgatggagcatcgatcgactgcagtcagtcgaat 1248
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LOCUS
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ACCESSION AX281095
VERSION AX281095.1 GI:16608362
KEYWORDS
SOURCE Physcomitrella patens.
ORGANISM Physcomitrella patens.
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
AUTHORS Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
1 (sites)
TITLE costa e Silva, O.D., Bohnert, H.J., van Thiel, N., Chen, R. and
Ishitani, M.
JOURNAL Signal transduction stress-related proteins and methods of use in
plants
PATENT: WO 0177355-A 1 18-OCT-2001;
BASF Plant Science GmbH (DE)
FEATURES
Location/Qualifiers
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/db_xref="taxon:3218"
BASE COUNT 198 a 178 c 201 g 183 t
ORIGIN

Query Match 19.7%; Score 422; DB 6; Length 760;
Best Local Similarity 74.0%; Pred. No. 1.6e-117;
Matches 549; Conservative 0; Mismatches 190; Indels 3; Gaps 1;

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9 CCAAGAAGGGGATTTGGCGCAGGATCTATTGGGGGATGTGTTCGACTTACAGCCGAGA 68
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Venkataraman,G., Reddy,M.K. and Sopory,S.K.				
Unpublished				
2 (bases 1 to 2113)				
Reddy,M.K				
Direct Submission				
Submitted (27-OCT-1997) M.K. Reddy, International Centre for				
Genetic Engineering and Biotechnology, Plant Molecular Biology Lab,				
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1739	ttcatgggcaccccaattggaaatgaggaccatgagtgtgcccctaaaaatgcctgagctcgc	1798
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DSA291467	2038 bp	linear	PLN 18-OCT-2000
LOCUS	DSA291467		
DEFINITION	Digitaria sanguinalis mRNA for phosphoinositide-specific phospholipase C (plc2 gene).		

ACCESSION AJ291467
 VERSION AJ291467.1 GI:10880264
 KEYWORDS phosphoinositide-specific phospholipase C; plc2 gene.
 SOURCE Digitaria sanguinalis
 ORGANISM Digitaria sanguinalis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 Penicillaceae; Digitaria.

AUTHORS
Coursol, S., Pierre, J.N., Vidal, J. and Grisvard, J.

JOURNAL Unpublished
2 (bases 1 to 2038)

TITLE	Direct Submission
1. THE	
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de Biotechnologie de
Location/Qu

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VADBNEDDILE

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complete cds.

2170 bp mRNA linear PLN 01-JUL-1996

U41475
U41475.1 GI:1399306

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Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

1 (bases 1 to 2170)
Sh,J., Gonzales,R.A. and Bhattacharya,M.K.
Phosphoinositide-specific phospholipase Cs contain a C-terminal
domain having homology to the C2 domain of protein kinase C

Unpublished
2 (bases 1 to 2170)

Clouse,J.A.
Direct Submission
Submitted (29-NOV-1995) Joe A. Clouse, The Samuel Roberts Noble
Foundation, Inc., Plant Biology Division, P.O. Box 2180, Ardmore,
OK 73402, USA

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 QY 1626 gcttttccaaacgcattttgacattctcaacttccacagattcttcaactaggtgatt 1685
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 QY 1686 gtggtggagtgctgctgaagagccaaagtggaagacattctgtgtgacaaattcatg 1745
 Db 1659 ATAGCGGAGTACACGAGCTCGTGATGAAGAGACGAGGCGGATAGAGATACATG 1718
 QY 1746 gacccccattgaatgaagaccattagtttgccttaaaatgcctgagctgcactactt 1805
 Db 1719 GTGCGGTGTTGGAGGAGGATTTTCACTTCAAACTGACCGTCCGCGGATCGGTGCTG 1778
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 Db 1779 CGGTGGAGGTGACGAGTACGACATGTCGGAGAGGAGGACTTCGGCGGCGCAGACGGT 1838
 QY 1866 ctcccatccatgaagtcgggagtggtatcggtgacaaatgtacgacaaagagggc 1925
 Db 1839 CTGCGGTGTCGAGCTCATCCCGGGATCCGAGCGGTGGCACTCCACGACCGCAAGGG 1898
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RESULT 14
NRPHOSLPC
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 N. rustica mRNA for phospholipase C. linear PLN 04-FEB-1999
 X95877.1 GI:1771380
 phospholipase C-specific phospholipase C.
 Aztec tobacco.
 Nicotiana rustica
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 Pical, C., Gray, J.E. and Hetherington, A.
 Unpublished
 2 (bases 1 to 2066)
 Pical, C.
 Direct Submission
 Submitted (26-FEB-1996) C. Pical, University of Sheffield,
 Molecular Biology and Biotechnology, PO Box 594, Sheffield, S10
 2UH, UK
 Revised by author 26-JUL-96
 3 (bases 1 to 2066)
 Pical, C., Kopka, J., Muller-Rober, B., Hetherington, A.M. and
 Gray, J.E.
 Isolation of two cDNA clones for phospholipase C-specific
 phospholipase C from epidermal peels (accession no. X95877) and
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 Plant Physiol. 114, 748-748 (1997)
JOURNAL
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 ORIGIN

Query Match 10.7%; Score 229.4; DB 8; Length 2066;
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 Matches 874; Conservative 0; Mismatches 766; Indels 105; Gaps 8;

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 Db 191 ATGAATTCAGAACAGTATTGAAATCTTGATTGAAGTACAAAGAGAGACCTTTTCACT 250
 QY 282 ctgtgacgcccagcagatcagcagcagcagcagcagcagcagcagcagcagcagcagc 341
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Sun Jul 28 10:34:38 2002

[illegible]

us-09-828-447-7.rge

Sun Jul 28 10:34:38 2002

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2002, 17:22:17 ; Search time 63.5 Seconds
(without alignments)
1710.879 Million cell updates/sec

Title: US-09-828-447-12
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phase.*
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 - 14: sp_unclassified.*
 - 15: sp_rvirus.*
 - 16: sp_bacteriap.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1253.5	37.7	588	10 P93341	P93341 nicotiana r
5	1251.5	37.6	600	10 Q43443	Q43443 glycine max
6	1249	37.5	593	10 Q93VX8	Q93VX8 medicago tr
7	1241.5	37.3	600	10 Q43439	Q43439 glycine max
8	1234	37.1	551	10 Q43444	Q43444 glycine max
9	1225.5	36.8	585	10 O49952	O49952 solanum tub
10	1225	36.8	591	10 Q940R9	Q940R9 arabidopsis
11	1225	36.8	597	10 Q940Y9	Q940Y9 arabidopsis
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14	1194	35.9	605	10 Q9M5Q2	Q9M5Q2 nicotiana t
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33	656.5	19.7	502	13 Q91423	Q91423 catfish, ph
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35	636	19.1	771	11 Q63693	Q63693 rattus norv
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37	628	18.9	641	6 Q95JS1	Q95JS1 macaca fasc
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DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)				
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)				
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OS	Glycine max (Soybean).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
OC	eurosid1 I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.				
OX	NCBI_TaxID=3847;				
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RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV. WILLIAMS 82; TISSUE=ETIOLATED HYPOCOTYLS;				
RA	Shi J., Gonzales R.A., Bhattacharyya M.K.;				
RT	"Phosphoinositide-specific phospholipase Cs contain a C-terminal domain having homology to the C2 domain of protein kinase C.";				
RL	Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.				
RL	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV. WILLIAMS 82; TISSUE=ETIOLATED HYPOCOTYLS;				
RA	Clouse J.A.;				
RL	Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.				
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DR	HSSP; P10688; 1DJH.				
DR	InterPro; IPR000008; C2.				
DR	InterPro; IPR001192; PI-PLC.				
DR	InterPro; IPR000909; PI-PLC_X.				
DR	InterPro; IPR001711; PI-PLC_Y.				
DR	Pfam; PF00168; C2; 1.				
DR	Pfam; PF00388; PI-PLC-X; 1.				
DR	Pfam; PF00387; PI-PLC-Y; 1.				
DR	PRINTS; PR00390; PHPLIPASEC.				
DR	ProDom; PD001202; PI-PLC_Y; 1.				
DR	SMART; SM00239; C2; 1.				
DR	SMART; SM00148; PLCXC; 1.				
DR	SMART; SM00149; PLCYC; 1.				

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DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50007; PIPIC_X_DOMAIN; 1.
DR PROSITE; PS50008; PIPIC_Y_DOMAIN; 1.
DR PROSITE; PS50008; PIPIC_Y_DOMAIN; 1.
SQ SEQUENCE 533 AA; 62937 MW; 691446828AF70687 CRC64;
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Query Match 40.2%; Score 1338; DB 10; Length 553;
Best Local Similarity 47.9%; Pred. No. 1.1e-84;
Matches 282; Conservative 85; Mismatches 176; Indels 46; Gaps 11;

QY	34	MSAEGLLKFLHTEGQDVDFTLDDAKOIMERIKRDKWKSFGIAST-----NSDLKSEAF	86
Db	1	MSADQILFLRHQHQRETCDAESDNRILDSIIOSRKQNDNAECDHHTDNNNGLSLDFE	60
QY	87	RKYLMMNDPLGVHLNVVHDMTPQMSHYFTTGHNSYLTGNSLSSDSDTPIAAALLRRGV	146
Db	61	FRFLFVDFNDPLKQSVHHDMNAPLSHYFTYTGHSYLTGNSLSSDSDVPITKALORGV	120
QY	147	RVVELDLWPDD-KGGMKVTHGNTLTNPVSPKQCVTAIKNAEFTSEYPCVVIIEHILTSE	205
Db	121	RVIELDLWPNSTRDDIDVHGRLTAPVSLIQCLCKSIKEYAFVKVSDVPVITIEHILTPF	180
QY	206	LOGHAAILBQILGDALYPTTDAIYVFPSPESLARKIIISTKPKKEYLEACSTOKLAM	265
Db	181	LOAKVAEMIAQVFGDMLYF-PQADSLTERPTPESIKGRILISTKPKKEYLES-----	231
QY	266	ENRNLVELEKEDKLEQTTFAPLEENHILIGENTPSPSRKEVEVLSOKEMSTPAELNSRSPS	325
Db	232	-----KQFKDSDSEREST-----EESLSPCVIPELEAVDEK-----LNG----	267
QY	326	DLGEATSTRYSKSDNGDNPKHFYKARLTIIRLAKHAKTSMHEHRLQVDESVKRLISLSES	385
Db	268	DLDEEGLNARDKKSDOOSAP--EYKRLTIIHAGK-PKG-HVKHHLNNVGGVKRLUSEQ	322
QY	386	KLEKVVKEUPEALVKETQNLIRVYPAANRVSNNSFCPTLAWNYGAQMVAAQMGYKSEL	445
Db	323	ELEKASATYGSQDITVRETOKNIIRVYPKGTRVTSNRYPHIGWYGAQMVAAQMGHGKSL	382
QY	446	WQAFGFKGNGGGYVLPQVILLENLPSCVGNPTSPRNTTILIKIKVYTTILGWDKAFSK	505
Db	383	WYMQGHFRANGCGYVYKFAFLEIEGPHNEVDFPKRALPVKKT LKVKYVMGNGWSSDFSK	442
QY	506	RHFDLSPPDFTRVIWGVPADEAKWKTSVVDNSWAPHNEDHEFALKCPCELLALLREV	565
Db	443	THFDSESPDFVTKVICVGPADKANKTKVIQDNWFPVWDEEFPFLTPVELALLREV	502
QY	566	ROHDDSDKDEFGQTCPLIHEVRDGYRCMQMDYKGNVGLKGVLMFLHFHQ	614
Db	503	REYDKHEKDDFGQGTCLPISLRGSRFVAPFLFDQKGQGLKSVKLLIMBFO	551

RESULT	2
P93620	
ID	P93620
AC	PRELIMINARY;
CC	PRT; 549 AA.
DT	01-MAY-1997
DT	(TRENBLrel. 03, Created)
DT	01-DEC-2001
DT	(TRENBLrel. 03, Last sequence update)
DT	01-FEB-2001
DT	(TRENBLrel. 19, Last annotation update)
DE	PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C
DE	(EC 3.1.4.11).

VORL1.
 Vigna unguiculata (Cowpea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
 OC eudicots I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
 NCBI_TaxID=3917;
 [1]
 RN SEQUENCE FROM N. A.
 RP STRAIN=CV. EPAGE-1; TISSUE=LEAF;
 RA Pham Thi A.T., El Maarouf H., Gareil M., d'Arcy-Lameta A.,
 RA Zully-Fodil Y.;
 RA "Molecular cloning and expression of a phosphoinositide-specific
 RT phospholipase C in Cowpea leaves.";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

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DR EMBL; U05250; AB041107.1; -.
DR HSP; P10688; 1DUJH.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001192; PI_PLC.
DR InterPro; IPR009090; PI_PLC_X.
DR InterPro; IPR001171; PI_PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00368; PI_PLC-X; 1.
DR Pfam; PF00387; PI_PLC-Y; 1.
DR PRINTS; P00390; PHPLIPASEC.
DR ProDom; PD001202; PI_PLC_Y; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00148; PLCXc; 1.
DR SMART; SM00149; PLCYc; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50007; PIPUC_X_DOMAIN; 1.
DR PROSITE; PS50008; PIPUC_Y_DOMAIN; 1.
DR Hydrolase.
KW SEQUENCE. 549 AA; 62281 MW; 19A833

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Query Match 38.9%; Score 1293; DB 10; Length 549;
Best Local Similarity 44.9%; Pred. No. 1.4e-81;
Matches 272; Conservative 85; Mismatches 157;

QY	12	PKGDPEQDLUGVEFTIYSEN-ERMSAEGLLKFLHTEQGDVDFTLDDAKQIMERIRK-DWK	69
Db	21	PKPPPD---VQKAFSEFSDGASSAHLLRFLAEHQGEVDCTVSDSEQILQOSRKEDGE	77
QY	70	KSFGLASINSDLSKEAFKRYLWNPDLGCVLHNVHQDMQTPMSHYFFTFCHNSYLTGNQL	129
Db	78	TCFDL-----HDFHFFLQENDLVNPLKSOVHHQDMNAPISHYFTYCHNSYLTGNQL	128
QY	130	SSDSOTPIAALRGVRVVELDLPD-DKGGMKVTHGNTLTNPVSQKCVTAIKNNAF	188
Db	129	SSDCSDAPIIKALQRGVRIELDLPWNSNKDDIDVHGRTLTTPVSLRLCLKSIKEYAFV	188
QY	189	TSEYPCVCTIEDHLTSELQGHAAEILQILDALYYPPTDALVEPSPESLKRKLIIST	248
Db	189	KSOYPLVITLEDHLPDLOAKVAKMAQVGGELLHY-PQDSTLTFPSPESLKRGLRILST	247
QY	249	KPKKEYLEACSTOKLAMENRNVEELEKEDKLEQTTAPLEENHILGENTPSLRKEVEYL	308
Db	248	KPKKEFLS-----	256
QY	309	SOKEMSTPAELNRSRPSDLGEATSTRYSKSDNGDNPKHFKYARLITIRLAKHAGTSM	368
Db	257	SEKESAE-----EVSLRENADQRTDNKRAPEYKRLITIHAGK-PKG-ELQ	301
QY	369	HLQWDSVVKRISLSESKLEKVVKEKPEALVKFTOKNILLRVYPAANRVNSSFPCPTLAWN	428
Db	302	DELKAAGNVRLSLEQALEKASESGYADVVRTHNNILRVYKPGTRLNSSFNYKPHIGMT	361
QY	429	YGAQWAAQNMGYKGEKLQWAFGFKGNGCGVYLKPOYLLENLPGVPFNPTSPRNTTLI	488
Db	362	YGAQWAFNMGHGKSLWYTMQGFNRGNGCGYKPKPNFLIQRGPDQDEVDPKIALPVKKT	421
QY	489	LKIKVMTTLGWDAFKSRHFDLPSPDFTFRLVGVGPDAEAKWTSVVDNNSWAPHNED	548
Db	422	LKVKVYLKGKWSLDFSPSDFSYSPDPFVYKVICVGPADMKKTSVISNNWFPVWNEE	481
QY	549	HEFALKCPALALLRIEVRDHDDSDKDFEGQCTCLPIHEVRDGYRCMQYDKGNVLKGV	608
Db	482	FDPLTVPIVALLIGIEVRDEDDKHQDDFGQCTCLPVSSELKSGFSRVPVLYDEKGYKSVK	541
QY	609	MLFHFQ	614
Db	542	LLMRFO	547

RESULT 3
O49902
ID O49902
PRELIMINARY;
PRT: 588 AA

us-09-828-447-12.rspt

Sun Jul 28 10:34:37 2002

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AC 049902;
DT 01-JUN-1998 (TREMELrel. 06, Created)
DT 01-JUN-1998 (TREMELrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE (EC
DE 3.1.4.11).
DE Nicotiana rustica (Asteraceae).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4093;
RN [1]
RP SEQUENCE FROM N.A.
RA Pical C., Kopka J., Muller-Rober B., Hetherington A.M., Gray J.E.;
RT "Isolation of two cDNA clones for phosphoinositide-specific
RT phospholipase C from epidermal peels (accession no. X95877) and guard
RT cells (accession no. Y11931) of Nicotiana rustica (PGR97-086).";
RL Plant Physiol. 114:748-748(1997).
DR EMBL; Y11931; CAA72681.1; -.
DR HSSP; P10688; 1DJH.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001192; PI-PLC.
DR InterPro; IPR000909; PI-PLC_X.
DR InterPro; IPR001711; PI-PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00388; PI-PLC-X; 1.
DR Pfam; PF00387; PI-PLC-Y; 1.
DR PRINTS; PR00390; PHPLIPASEC.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
DR Hydrolase. 588 AA; 66942 MW; C132712EE2E1220E CRC64;
KW SEQUENCE
SQ
Query Match 37.8%; Score 1259.5; DB 10; Length 588;
Best Local Similarity 44.0%; Pred. No. 3.3e-79;
Matches 267; Conservative 94; Mismatches 203; Indels 43; Gaps 12;
QY 13 KGDPQDLVGEVFTIYSEN-ERMSAEGLLKFLTEQGDVDFTLDDAKQIMERIRKDWKS 71
DB 18 EAEPPSD-VKEAFKKAENGQNMSEQLLKFLIEVQGETLFTVGDSVDI---VRQILQKR 73
QY 72 FGLAST-NSDLSKEAFKRYLNPDLNGLVHNVHODMTQPMASHYFTFTGHSNLTGNQLS 130
DB 74 HPITKLTROTALAEDEHFLFNTDLPNPPINKVHHDNMAPLSHYFTFTGHSNLTGNLT 133
QY 131 SDSSTPIAAALRGVRVVELDLWPD-DKGMKVTHGNTLTNPVSFOKCVTAIKNAFFT 189
DB 134 SDSDVPIKALKKGVRIELDWPNKDDIHVLHGRTVTPVELIRCLSKIKEHAFVA 193
QY 428 NYGAQVMAQNGYGRALWLMHGMFRSNGCGYKVPDFLLNVPNNNEVDFPKAKLPVK 459
QY 488 ILKIKVMTTLGWDAKSKRHFDFSPDFTRVIVGVPADEAKWKSVVDNSWAPHWNE 547
DB 460 TLKVKVVMGSGWHLDFKQTHFDLYSPDFYTRVGIAGVPADEIMKTKTKEDKTPWDE 519
QY 548 DHEFALCPALALRIEVRHDDSDKDEFGOTCLPIHEVRDGRYRCMQMYDKKGNLVKGV 607
DB 520 AFTEPLTVPELALLRIEVRHDDSDKDEFGOTCLPIHEVRDGRYRCMQMYDKKGNLVKGV 579
QY 608 LMLHFQ 614
DB 580 RLIMRFE 586
RESULT 4
ID P93341 PRELIMINARY; PRT; 588 AA.
AC P93341;
DT 01-MAY-1997 (TREMELrel. 03, Created)
DT 01-MAY-1997 (TREMELrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C.
OS Nicotiana rustica (Asteraceae).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4093;
RN [1]
RP SEQUENCE FROM N.A.
RA Pical C., Kopka J., Muller-Rober B., Hetherington A.M., Gray J.E.;
RT "Isolation of two cDNA clones for phosphoinositide-specific
RT phospholipase C from epidermal peels (accession no. X95877) and guard
RT cells (accession no. Y11931) of Nicotiana rustica (PGR97-086).";
RL Plant Physiol. 114:748-748(1997).
DR EMBL; X95877; CAA65127.1; -.
DR HSSP; P10688; 1DJH.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001192; PI-PLC.
DR InterPro; IPR000909; PI-PLC_X.
DR InterPro; IPR001711; PI-PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00388; PI-PLC-X; 1.
DR PRINTS; PR00390; PHPLIPASEC.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
DR SEQUENCE 588 AA; 66765 MW; 4CC0338AA3DA61C4 CRC64;
SQ
Query Match 37.7%; Score 1253.5; DB 10; Length 588;
Best Local Similarity 44.0%; Pred. No. 8.6e-79;
Matches 267; Conservative 94; Mismatches 203; Indels 43; Gaps 13;
QY 13 KGDPQDLVGEVFTIYSEN-ERMSAEGLLKFLTEQGDVDFTLDDAKQIMERIRKDWKS 71
DB 18 EAEPPSD-VKEAFKKAENGQNMSEQLLKFLIEVQGETLFTVGDSVDI---VRQILQKR 73
QY 72 FGLAST-NSDLSKEAFKRYLNPDLNGLVHNVHODMTQPMASHYFTFTGHSNLTGNQLS 130
DB 74 HPITKLTROTALAEDEHFLFNTDLPNPPINKVHHDNMAPLSHYFTFTGHSNLTGNLT 133
QY 131 SDSSTPIAAALRGVRVVELDLWPD-DKGMKVTHGNTLTNPVSFOKCVTAIKNAFFT 189
DB 134 SDSDVPIKALKKGVRIELDWPNKDDIHVLHGRTVTPVELIRCLSKIKEHAFVA 193
QY 190 SEYPCVCTIEDHLTSELOHAAEILQILGDALYTPPTDAILVEPPSPESLKRILISTK 249

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Db 194 SPYVITLEDHLPDLOAKVAQMLTETEGEMLFV-PSDSLKCEPTPEELKHLRIISTK 252
 QY 250 PPKYLEACSTOKLAMENRNVLVEELEKEDKLEQTTFAPLEENHILGENTPISLRKEVEVLS 309
 Db 253 PPKYLEACSTOKLAMENRNVLVEELEKEDKLEQTTFAPLEENHILGENTPISLRKEVEVLS 309
 QY 310 OKEMSTPAELNSRSPDGEATSTRYSKNDGNDNPK-HFKYARLITIRLAKHAKGTSME 295
 Db 296 OEB-----NEKSDS-----NFEDDDSSHRPOLASAYKRLIAHAGKPKGG-LK 339
 QY 369 HRLQVD-ESVKRISLSSEKLEKVEKPEALVFTQKNILRVYPAANRVNSNFCPTLAW 427
 Db 340 EALKVDPKVRLSLSEQALKAESAESHGTEIVRTQKNILRVYPAANRVNSNFCPTLAW 427
 QY 428 NYGAQVAQNMGGYKGLWQAFKFGKGGYVLPKPOYLENLPSPVFPNFTSPRNTTL 399
 Db 400 MHGAQMAVFNMGYGRALWLMHGMFSSNGCGYVLPKPOYLENLPSPVFPNFTSPRNTTL 487
 QY 488 ILKIKVMTTLGWDAFKSKRHFDFSPDPFTRVIVGVPADEAKWKTSVVDNSWAPHWNE 459
 Db 460 TLKVKVYMGDGHLDKQTHFDLYSPDFYTRVGIAGVPADEAKWKTSVVDNSWAPHWNE 547
 QY 548 DHEALCAPALALRIEVRDHDSDSKDEFEGQTCPLPIHEVRDGYRCQMVDKKNVLPKW 519
 Db 520 EFTFPLVPEALLRIEVRDHDSDSKDEFEGQTCPLPIHEVRDGYRCQMVDKKNVLPKW 607
 QY 608 LMLFHFQ 614
 Db 580 RLLMRF 586

RESULT 5
 Q43443 PRELIMINARY; PRT; 600 AA.
 ID Q43443
 AC Q43443
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DE PHOSPHONOSITIDE-SPECIFIC PHOSPHOLIPASE C P13.
 OS Glycine max (soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 RN NCBI_TaxID=3847;
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. WILLIAMS 82; TISSUE=ETIOLATED HYPOCOTYLS;
 RA Shi J., Gonzales R.A., Bhattacharyya M.K.;
 RT "Phosphonositide-specific phospholipase Cs contain a C-terminal
 RL domain having homology to the C2 domain of protein kinase C.";
 RN Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. WILLIAMS 82; TISSUE=ETIOLATED HYPOCOTYLS;
 RA Clouse J.A.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U41474; AB03258.1; -;
 DR HSSP; P10688; LDJH.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR001192; PI_PLC.
 DR InterPro; IPR000909; PI_PLC_X.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00387; PI_PLC-X; 1.
 DR PRINTS; PR00390; PHPLIPASEC.
 DR PRODOM; PD001202; PI_PLC_Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00148; PLCYC; 1.
 DR SMART; SM00149; PLCYC; 1.
 DR PROSITE; PS50004; C2_DOMAIN.2; 1.
 DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.

DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
 SQ SEQUENCE 600 AA; 68696 MW; EC1778F1BB3B27ED CRC64;

Query Match 37.6%; Score 1251.5; DB 10; Length 600;
 Best Local Similarity 45.8%; Pred. No. 1.2e-78;
 Matches 272; Conservative 89; Mismatches 202; Indels 31; Gaps 12;
 QY 24 VFTIYSNERMSAEGLLKFLHTEQGDVFTLDDAKOIMIRKDKWKSGFLGASINDSLK 83
 Db 31 LFEYSENELMPTSHLRELVDVQROEKATEDAQAIIDSFRHFRGAG-----LNL 83
 QY 84 EAFKRYLMPDNLGV-LHNVDQMTQPMSHYFTGHNSYLTGNLSLSSDSTPIAAL 142
 Db 84 EFTFKYFDDDDPPLPSHGVDHMTPLSHFYTYGHNSYLTGNLSLSSDSTPIAAL 142
 QY 143 RRGVRVVELDLWD-DKGMKVTHGNTLTPVSKQCVTAIKNAFTSEYVPCVTIEDH 201
 Db 144 KKGVRVIELDIWPNASKDSIDLHGRTLTTPVELIRLSIKDHAFVASEYPVVITLEDH 203
 QY 202 LPSLOGHAAEILQILGDALYPPPTDALVEFPSPESLKRKIIISTKPKYLEACSTQ 261
 Db 204 LTPDLQAKVAEMVTQTGDL-ETPNSESVKEFPSPESLKRKIIISTKPKYLEACSTQ 261
 QY 262 KLAMENRNVLVEELEKEDKLEQTTFAPLEENHILGENTPISLRKEVEVLSQEMSTPAELNS 321
 Db 263 K-----GDSQHEKEKGGDSEHGKAS--GEDEAGKEVPSL-KGSTIEDYKONNVDELND 315
 QY 322 RSPDLGEATSTRYSKNDGNDNPKHFKYARLITIRLAKHAKGTSMEHRLQVD-ESVKRI 380
 Db 316 EEEFD-----ESDKSHNEAP---EYRHLIAHACK-PKGLIVE-CLKVDEPKVRL 362
 QY 381 SLSEKLEKVEKPEALVKFTQKNILRVYPAANRVNSNFCPTLANNYGAQVAQNMGG 440
 Db 363 SLSEQOLEKAAINYGOQIVRFTQKNILRVYPAANRVNSNFCPTLANNYGAQVAQNMGG 440
 QY 441 YGKELWQAFKFGKGGYVLPKPOYLENLPSPVFPNFTSPRNTTLILKIKVMTTLGWD 500
 Db 423 YGRSLWLMHGMFRANGCGYVLPKPOYLENLPSPVFPNFTSPRNTTLILKIKVMTTLGWD 500
 QY 501 KAFSKHFDLPSPDPFTRVIVGVPADEAKWKTSVVDNSWAPHWNEDEHEFALKCPAL 560
 Db 483 YDFKTHFDQSPDPFTRVIVGVPADEAKWKTSVVDNSWAPHWNEDEHEFALKCPAL 560
 QY 561 LRIEVRDHDSDSKDEFEGQTCPLPIHEVRDGYRCQMVDKKNVLPKWLMFHFQ 614
 Db 543 LRIEVRDHDSDSKDEFEGQTCPLPIHEVRDGYRCQMVDKKNVLPKWLMFHFQ 596

RESULT 6
 Q93YX8 PRELIMINARY; PRT; 593 AA.
 ID Q93YX8
 AC Q93YX8
 DT 01-DEC-2001 (TREMELrel. 19, Created)
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
 DE PHOSPHONOSITIDE-SPECIFIC PHOSPHOLIPASE C.
 GN PLC1.
 OS Medicago truncatula (Barrel medic).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
 RN NCBI_TaxID=3880;
 RP SEQUENCE FROM N.A.
 RC Engstrom E.M., Long S.R.;
 RT "MEPLC1, a putative phosphoinositide-specific phospholipase C from
 RL Medicago truncatula.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY059631; AAL17948.1; -;
 SQ SEQUENCE 593 AA; 67419 MW; AA37967169DAB4A5 CRC64;

reference: J. A. :
 ... /compark /nrbj databases.

CL	Closure J.A.;
EMBL	Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
HSSP	U25027; AAA74441.1; -;
InterPro	P10688; 1DJH.
InterPro	IPR000008; C2.
InterPro	IPR001192; PI_PLC.
InterPro	IPR000909; PI_PLC_X.
InterPro	IPR001711; PI_PLC_Y.
pfam	PF00168; C2; 1.
pfam	PF00388; PI_PLC-X; 1.
pfam	PF00387; PI_PLC-Y; 1.
PRINTS	PR00390; PPHPLIPASEC.
PRODOM	PD001202; PI_PLC_Y; 1.
SMART	SM00239; C2; 1.
SMART	SM00148; PLCXC; 1.
SMART	SM00149; PLCYC; 1.
PROSITE	PS50004; C2_DOMAIN_2; 1.
PROSITE	PS50007; PIPLC_X_DOMAIN; 1.
PROSITE	PS50008; PIPLC_Y_DOMAIN; 1.
SEQUENCE	600 AA, 68798 MW, 2BACC5A4DB54BE1D CRC64;

Query Match	37.3%; Score 1241.9; EE 21;	
Best Local Similarity	45.3%; pred. No. 6e-78;	
Mismatches	205;	Indels 31; Gaps 11;
Conservative	89;	

[illegible]

RESULT	8
ID	Q43444 PRELIMINARY; PRT; 551 AA.
AC	Q43444; 1996 (T-EMBLrel. 01, Created)
DT	01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DD	01-NOV-1996 (T-EMBLrel. 01, Last sequence update)

[illegible]

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RESULT 7
ID Q43439 PRELIMINARY: PRT: 600 AA.
AC Q43439; 1996 (T-EMBLrel. 01, Created)
AC 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
AC 01-NOV-1996 (T-EMBLrel. 19, Last annotation update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C.
DE Glycine max (Soybean);
DE Glycine max (Soybean);
DE Eukaryota; Viridiplantae; streptophyta; tracheophyta;
DE Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
DE eucotids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OC NCBI_TaxID=3847;
OX NCBI_TaxID=3847;
RN [1]
RN SEQUENCE FROM N.A.
RN STRAIN=CV. WILLIAMS 82; TISSUE=ETIOLATED HYPOCOTYLS;
RN STRAIN=CV. WILLIAMS 82; TISSUE=ETIOLATED HYPOCOTYLS;
RX MEDLINE=96045546; PubMed=7550376;
RX Shi J., Gonzales R.A., Bhattacharyya M.K.;
RA "Characterization of a plasma membrane-associated phospholipase C from soybean.";
RT "Specific phospholipase C from soybean.";
RT Plant J. 8:381-390(1995).
RL [2]
RN SEQUENCE FROM N.A.
RN STRAIN=CV. WILLIAMS 82; TISSUE=ETIOLATED HYPOCOTYLS;
RN STRAIN=CV. WILLIAMS 82; TISSUE=ETIOLATED HYPOCOTYLS;

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QY 253 EYLEACSTOKLAMENRNLVELEKEDKLEQTFAPLEENHILGENTPSLRKEVEVLISOKE 312
|||:|
Db 256 EYLOA-----KEVNETGAMKGT-----QTFEANGREV 284
|||:|
QY 313 MSTPAELNSPSDLGA-TSTRYKSNNGNDNPKHKFYARLITIRLAKHAKGTSMEHRL 371
|||:|
Db 285 SDIKARYNDKDDSEGAADSDDEEDPTSQONTAP---EYRLIAIHAGKGGGLS--DWL 339
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QY 372 QVD-ESVKRLSLESKLEKVEKWPALYKFTOKNLRVYPAANRVNSNFCPTLAWNTG 430
|||:|
Db 340 RVPDKVRRRLSSEQLGKAVVTHGKEIRFTQRTNLRIRYPKGIREDSSNPFNAWTHG 399
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QY 431 AQVAAQNMCGYGRKELWQAFKFGKNGCGYVLPQVLLNLPSPGVNPTS--PRNTTLI 488
|||:|
Db 400 AQVAFNMCGYGRSLMLHMGFRNGCGYVKKPDILLKAGPNNEVDFPEANLPVKTT-- 457
|||:|
QY 489 LTKVMTTLGWDAKAFKRHDFLSPDPFTTRVIVGVPADEAKWKTSVVDNSWAPHNED 548
|||:|
Db 458 LKTVFMGEGWYDFETHFDAYSPPDFYARIGIAGVDADIVMKTKTLEDNWIPTWDEQ 517
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QY 549 HEFALCPALALRIEVRHDDSDKDFEFGQTCPLPIHEVRDGYRCMQTKGKGNVLKGV 608
|||:|
Db 518 FEPLTVPELALLURVEHYDMSKDDFAGQTCPLVSELROGIRAVPLHNRKGEKYNYSK 577
|||:|
QY 609 MLFHFQ 614
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Db 578 LLRLFE 583
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RESULT 10
Q940R9 PRELIMINARY; PRT; 591 AA.
ID Q940R9;
AC Q940R9;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE PHOSPHINOSITIDE-SPECIFIC PHOSPHOLIPASE C4.
OS Arabidopsis thaliana (Mouse-ear cress).
GN PLC4.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Pical C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY053422; AAL23439.1; -.
SQ SEQUENCE 591 AA; 67335 MW; 67CC1169F422BE22 CRC64;

Query Match 36.8%; Score 1225; DB 10; Length 591;
Best Local Similarity 43.4%; Pred. No. 8.3e-77;
Matches 269; Conservative 101; Mismatches 206; Indels 44; Gaps 13;

QY 2 CSIACRSTPKGDPQDQVIVGVFTTYIGENE-RMSAEGLLKFLHTEQGDVDFTLDDAKQI 60
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Db 7 CLIFTRKFRMTESGPVED-VRLDFEKYTEGDAHMSPEQLQKLMTTEGEGEGETSLEAE 65
|||:|
QY 61 MERIRKDWKSGLASINSLSKAFKRYLMPDLNGLVHNVHVDMPQMSHFIPTGTH 120
|||:|
Db 66 DEVLR--RKHHIAKTRNLDFNFYLFSTDLNPIAQVHQNMDAPLSHYFIPTGTH 123
|||:|
QY 121 NSYLTGNOLSSSDPTIAAALRRGVVVELDLPDDPKGGMKVTGNTLTPVSPFOKCVT 180
|||:|
Db 124 NSYLTGNOLSSNCSELPIDALRRGVVVELDLPDDPKGGMKVTGNTLTPVSPFOKCVT 183
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QY 181 AKNNAFTTSEPCVCTIEDHLSLOQHAFILEQILGDALYYPPTFDALVEPPSPESL 240
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Db 184 SIKANAFATSKYPVITLEDHLTPKLOPKVAKMITQTFGDMLYY-HDSQCGQEPSPPEL 242
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QY 241 KRKLIISTKPPKYLEACSTOKLAMENRNLVELEKEDKLEQTFAPLEENHILGENTPS 300
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Db 243 KKKLIISTKPPKYLEA-----NDTKEKNGKGDSD-----DEDVWG----- 280
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QY 301 LRKEVEVLSQKEMSTPAELN--SRSPDLGEATSTRYKSNNGNDNPKHKFYARLITIRL 358
|||:|
Db 281 --KEPEDL-----ISTQSDLDKVTSSVNDLNQDDEERGSCEDTSQOLQAPVKRLIAHA 334
|||:|
QY 359 AKHAGTSMHELRQVD-ESVKRLSLESKLEKVEKWPALYKFTOKNLRVYPAANRVN 417
|||:|
Db 335 GKPKGGLRM--ALKVDPNKRIRLSLEQLLEKAVASYGADVIREFTQKNFLRIYPKGTRFN 392
|||:|
QY 418 SENFCTPLTAWNYGAQWVAONMCGYKELWQAFKFGKNGCGYVLPQVLLNLPSPGVNPTS 477
|||:|
Db 393 SSNYRFPQIGWMSGAGMIAFNMGYGRALWLMGFRANGCGYVKKPDILLMDASPNGQDF 452
|||:|
QY 478 NP---TSPRNTTLILKIKVMTTLGWDAKAFKRHDFLSPDPFTTRVIVGVPADEAKWKT 534
|||:|
Db 453 YPKDSSPKKT---LKVKVCMDGWLDFKKTHTFDSYSPDPFFVVRVGTAGAPVDEWMEKT 509
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QY 535 SVVDNSWAPHNEDHEFALCPALALRIEVRHDDSDKDFEFGQTCPLPIHEVRDGYRCM 594
|||:|
Db 510 KLEYDTWTPIWNKEFTFPPLAVPELALLRVEVHEHDVNEKDDFGGQTCPLVSEIRQGI 569
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QY 595 QMYDKKGNVLKGVLMFLHFQ 614
|||:|
Db 570 PLFNEKGVKYSTRLLMRFE 589
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RESULT 11
Q9LUY9 PRELIMINARY; PRT; 597 AA.
ID Q9LUY9;
AC Q9LUY9;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE PHOSPHINOSITIDE-SPECIFIC PHOSPHOLIPASE C.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Sato S.; Nakamura Y.; Kaneko T.; Katoh T.; Asamizu E.; Kotani H.;
RA Tabata S.;
RL "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
DR features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones."
RT DNA Res. 7:31-63(2000).
DR EMBL; AB020755; BAA97338.1; -.
DR HSP; P10688; IDJH.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001192; PI_PLIC.
DR InterPro; IPR000909; PI_PLIC_X.
DR InterPro; IPR001711; PI_PLIC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00388; PI-PLIC-X; 1.
DR Pfam; PF00387; PI-PLIC-Y; 1.
DR PRINTS; PR00390; PHPLIPASEC.
DR PRODOM; PD001202; PI_PLIC_Y; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00148; PLCXC; 1.
DR SMART; SM00149; PLCYC; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
SQ SEQUENCE 597 AA; 68038 MW; 176D1715653AF82B CRC64;

Query Match 36.8%; Score 1225; DB 10; Length 597;
Best Local Similarity 43.4%; Pred. No. 8.4e-77;
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OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eudicots II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. WESTAR;
 RA Das S., Hussain A.K., Keller W.A., Georges F.;
 RT "Isolation and characterization of a full cDNA coding region for
 RT phosphoinositide-specific phospholipase C from *Brassica napus*, cv.
 RT Westar.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF108123; AAD26119.1; -;
 DR HSP; P10688; IDJH.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR001192; PI-PLC.
 DR InterPro; IPR000909; PI-PLC_X.
 DR InterPro; IPR001711; PI-PLC_Y.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00388; PI-PLC-X; 1.
 DR Pfam; PF00387; PI-PLC-Y; 1.
 DR PRINTS; PR00390; PHPLIPASEC.
 DR ProDom; PD001202; PI-PLC_Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00148; PLCXC; 1.
 DR SMART; SM00149; PLCYC; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
 DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
 SQ SEQUENCE 581 AA; 66274 MW; 3E98CF88F7EAD7DE CRC64;

Query Match 36.1%; Score 1202.5; DB 10; Length 581;
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 Matches 269; Conservative 90; Mismatches 174; Indels 73; Gaps 17;

QY 21 VGEVFTIYSENERMSAEGLLKFLHTBOGDVFTLDDAKOIMERIRKDWKKSFGGLASI--N 78
 DB 27 VKTLEKYSENGWMTVDHLQRLIDVQKDKATKEDASIIIN-----AASSLLHS 76
 QY 79 SDSLKFAFRKYL---NPDLGVHNVHVDQTPMSHYFTFTGHSYLTGNQLSSDSS 135
 DB 77 NGHLDAFFKYLFGDSNPPL--ALHE-VHODMDAPISHYFTFTGHSYLTGNQLSSDSC 133
 QY 136 TPIAAALRGVRVVELDLPD--DKGKMKVTHGNTLTNPVSFOKCVTAIKNNAFTSEYPV 194
 DB 134 VPIIDALKGVRVVELDLPD--DKGKMKVTHGNTLTNPVSFOKCVTAIKNNAFTSEYPV 193
 QY 195 CVTIEDHLSLQGHAAEILEQILGALYPPPTDAPLHNTGTPMSHYFTFTGHSYLTGNQLSSD 254
 DB 194 VTTLEDHLPQLSKVAEMVTEIFGEILFTPPVGSLEKFPSPSLKRIIISTKPKPEY 253
 QY 255 LEACSTOKLAMENRNLVEELEKEDLEQTTAPLEENHILGENTPSPSRKEVEVLSQKMS 314
 DB 254 KEG-----KDEVDVQKGA-LGDEEVGVREVPSPF----- 281
 QY 315 TPAELN--SRSPDGLGEATSTRYSKNDGNDNPKHF-----YARLTIIRLAKHAKGTSM 367
 DB 282 --IERKSGDKDLDL-----EEDNDEDDVEFKKNAPQYKHLTAIAGK--PKG-SI 331
 QY 368 EHRLOYD--ESVKRISLSSEKLEKVVKEWPEALVKFTQKNILRVYPAANRVNSSFNFCPTLA 426
 DB 332 TACLAVDPDKVRRLSLSELEKAAEYAKQIVRFTQOONLRIYKPKTRVTSNNYPLVG 391
 QY 427 WNYGQAMVAQNMGGYKGLWQAFKFGKNGCGGVLPQVLLNPLSGVFPNP--TSRPN 484
 DB 392 WSHGQAMVAFNQYGRSLWLMQGMFRANGCGGYKPKPDLILKGGSDSIDFPKTIIPVK 451
 QY 485 TTLILKIKVMTLWGDKAFSKRHFDFLSPDPDFTRVTVWGVPADEAKWTSVVDNSWAPH 544
 DB 452 TT--LRVTIYMEGWYDFRTHFDQYSPDPDFYTRVGIAGVPADYVMKTKTLEDNWVFS 509
 QY 545 WNEDEHFAKCPALALLRIEVRDHDHDSKDFEFQGTCLPIHEVRDGRVRCMQYDKKGNVL 604
 DB 545 WNEDEHFAKCPALALLRIEVRDHDHDSKDFEFQGTCLPIHEVRDGRVRCMQYDKKGNVL 604

Db 510 WDEVFEPLTYPEALLRLLEVEHYDMSEKDDFGGQTCLPVWELQEGIRSFPLHNRKEEY 569
 QY 605 KGVLM 610
 DB 570 KSVKLL 575
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 ID Q9M5Q2 PRELIMINARY; PRT; 605 AA.
 AC Q9M5Q2;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE PHOSPHOLIPASE C2.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Goswami M., Singh B.N., Reddy M.K., Sopory S.K.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF223573; AAF33824.1; -;
 DR HSP; P10688; IDJH.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR001192; PI-PLC.
 DR InterPro; IPR000909; PI-PLC_X.
 DR InterPro; IPR001711; PI-PLC_Y.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00388; PI-PLC-X; 1.
 DR Pfam; PF00387; PI-PLC-Y; 1.
 DR PRINTS; PR00390; PHPLIPASEC.
 DR ProDom; PD001202; PI-PLC_Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00148; PLCXC; 1.
 DR SMART; SM00149; PLCYC; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
 DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
 SQ SEQUENCE 605 AA; 68634 MW; 1B8FAB26D1C64A50 CRC64;

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QY 21 VGEVFTIYSENERMSAEGLLKFLHTBOGDVFTLDDAKOIMERIRKDWKKSFGGLASIN-- 78
 DB 27 VKNLFKYSNGVMNAENLQRLIEVQKEENSSIEDAGGINNLH-----DKILNIF 79
 QY 79 --SDLSKFAFRKYL---NPDLGVHNVHVDQTPMSHYFTFTGHSYLTGNQLSSD 133
 DB 80 HRRGLDAFFKYLFPADINPPINP--KGIHDMNEPLSHYFTFTGHSYLTGNQLSSD 137
 QY 134 SDTPIAAALRGVRVVELDLPD--DKGKMKVTHGNTLTNPVSFOKCVTAIKNNAFTSEY 192
 DB 138 SDVPIIQAALRGVRVVELDLPD--DKGKMKVTHGNTLTNPVSFOKCVTAIKNNAFTSEY 197
 QY 193 PVTIEDHLSLQGHAAEILEQILGALYPPPTDAPLHNTGTPMSHYFTFTGHSYLTGNQLSSD 252
 DB 198 PVTIEDHLSLQGHAAEILEQILGALYPPPTDAPLHNTGTPMSHYFTFTGHSYLTGNQLSSD 255
 QY 253 EYLEACSTOKLAMENRNLVEELEKEDLEQTTAPLEENHILGENTPSPSRKEVEVLSQKE 312
 DB 256 EYLOA-----KEVKEKDS--KRGTDAP-----DTEAMGREVSDLK--- 288
 QY 313 MSTPAELNRSRSPDGLGEATSTRYSKNDGNDNPKHF-----KYARLTIIRLAKHAKGTSMEH 369
 DB 289 ---ARYNDKDDSDGAGVED--DESDGDPNSQNVAPYKCLIAIHAGKGGGLS--D 340
 QY 370 RLOYD--ESVKRISLSSEKLEKVVKEWPEALVKFTQKNILRVYPAANRVNSSFNFCPTLAWN 428

Db		79	GLQDGFENCLFSDVNPPLDPKLG--IHHDNNAPLSHVYIYTGHSYLTAGNQLSDCDDI	136
QY		137	PIAALRRGVVRVVELDWDPD-DKGOMKVTGHTLITNPVFSQKCVTAIKKNAFFETSEYPVC	195
Db		137	PLIQAQRSVRIEIDWPNSSDKDIEVLHGRTITAPVALIKRISIKEHAFSASEYPW	196
QY		196	VTIEDHLTSELQGHAAEILEQILGDALVYPTTDALVEFFSPESLARKKIIITKPKPKYL	255
Db		197	ITLEDHLITPDQEKVAEMITQFGDMLFSP--SESLKELSPESLKRKVMISTKPKPKYL	254
QY		256	EACSTQKLAMENRNRLVELEKEDKLEQTTFAPLENIHIGENTPSLRKEVEVLSOKEMST	315
Db		255	QS----REVKEKDTTKEAQDDVDDE-----BEDE-----	280
QY		316	PAELNSRSPDLGEMASTRYKSXSDGNDONPKHF-----YARLITIRLAKHAKGTSMHR	370
Db		281	-----DEDEDEEDPKSEKKAASEYKRLIIAHGKGGGLS--DW	318
QY		371	LOVD--ESVKRISLSESKLEKRVKEKWPALVKFTQKNILRVYPAANRVNNSNFCPTLANNY	429
Db		319	LKVDLUNKVRUSLSEPELEKANVTHSKETIIRITQGNLLRIYPKGI RVDSSNDYDPFVGMMH	378
QY		430	GAQMVAQNMQGYGKELMOAFKFGKNGGGYVLPQYLLLENLPGSVDFNPPTS--PRNTLT	487
Db		379	GAQMVAFNMQGYGRSLMLHMGFMFRANGGGYVKKPDLLLKAGPNNEVDFDTANLPVKTT--	437
QY		488	ILKIKVMTTLGWDAFKSKRHFDFLSPDPFTRVIVGVGPADAEAKWKTSVVVDNSWAPHNE	547
Db		438	-LKVTVMYMGDWKDFDQFOTHTDYSPPDYSYAKGLIAGVPADEVKRYKRTWDDNNIFSWDE	496
QY		548	DHEFAKCPPELALLRIEVRHDDDDSKDEFEGOTCLPIIHEVRDGYRCHQMXYDKKGNVLKV	607
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QY		608	LMLFHFQ 614	
Db		557	KLIMRFE 563	

Search completed: July 26, 2002, 17:29:21
Job time: 424 sec

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429	YGAQVAAQNMGGVGLGQAQFKPKNGCGGYVLKPOYLLLENLPSGVFPNPPTS--PRNIT	486
401	HGAQVAFNMGGVGRSLWLMHGFRSNGCGGYVKPKDILLKAGPNQIQIDPEANLPVKTT	460
487	LILKIKYMTTGLGDKAFSKRRHFDLSPDPFFTRVIVGVGVPADAKWKTSVVDNSWAPHNW	546
461	--LKVTVMGEGWYDFNTHETDAYAPDFVAKIAGVPADNMVKKTRTLENNWPTWD	518
547	EDHEFALKCPDELALLRIEVRDHHDDSKDEFFGQCTCLPIHEVRGRCYRCOMQYDKKGNVLKG	606
519	EKFEFLTPVETALLRVEVHVYDMSEKDDFAGQCTCLPVSSELRQGIKRAVSLHDKRGGRYS	578
607	VLMLEHFH 613	
579	VKLLMRF 585	
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01-JUN-1998	(TREMBLrel. 06, Last sequence update)	
01-DEC-2001	(TREMBLrel. 19, Last annotation update)	
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PLC2.		
Solanum tuberosum (Potato).		
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.		
NCBI_TaxID=4113;		
[1]		
SEQUENCE FROM N.A.		
MEDLINE=98111496; PubMed=9449844;		
Kobak J., Pical C., Gray J.E., Mueller-Roeber B.;		
"Molecular and enzymatic characterization of three phosphoinositide-		
specific phospholipase C isoforms from potato."		
Plant Physiol. 116:239-250(1998).		
EMBL; X94183; CAA63893.1; "		
HSSP; P10688; 1DJH.		
InterPro; IPR000008; C2.		
InterPro; IPR000413; Integrin_alpha.		
InterPro; IPR001192; PI_PLC.		
InterPro; IPR000909; PI_PLC-X.		
InterPro; IPR001711; PI_PLC-Y.		
Pfam; PF00168; C2; 1.		
Pfam; PF00388; PI_PLC-X; 1.		
Pfam; PF00387; PI_PLC-Y; 1.		
PRINTS; PR00390; PPHPLIPASEC.		
ProDom; PD001202; PI_PLC_Y; 1.		
SMART; SM00239; C2; 1.		
SMART; SM00148; PLCXc; 1.		
SMART; SM00149; PLCyc; 1.		
PROSITE; PS00004; C2 DOMAIN_2; 1.		
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us-09-828-447-12.rag

Sun Jul 28 10:34:35 2002

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 26, 2002, 16:05:57 ; Search time 50.59 seconds
(without alignments)
1378.817 Million cell updates/sec

Title: us-09-828-447-12

Perfect score: 3328

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues 747574

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1105	33.2	561	AA91932	Phosphatidylinositol
2	698.5	21.0	736	AA91932	Human phospholipase
3	698.5	21.0	789	AA91932	Amino acid sequenc
4	695	20.9	787	AA91932	Novel human phosph
5	650.5	19.5	736	AA91932	Novel human diagno
6	594.5	17.9	736	AA91932	Rat phospholipase
7	559	16.8	1096	AA91932	Inositol-1,4,5-tri
8	545.5	16.4	677	AA91932	Human protein sequ
9	543	16.3	217	AA91932	Arabidopsis thalia
10	508.5	15.3	1809	AA91932	Human phospholipase
11	501	15.1	1058	AA91932	Human protein SEQ

12	501	15.1	1216	22	AA91932	Human protein SEQ
13	474	14.2	1236	22	AA91932	Drosophila melanog
14	464.5	14.0	1312	22	AA91932	Arabidopsis thalia
15	430	12.9	178	21	AA91932	S. cerevisiae Plc1
16	428	12.9	869	15	AA91932	Human CG121 (or C5
17	418	12.6	567	22	AA91932	Arabidopsis thalia
18	414	12.4	173	21	AA91932	Phospholipase C-ga
19	409.5	12.3	1290	17	AA91932	Human protein sequ
20	344	10.1	306	22	AA91932	Human protein sequ
21	337.5	9.4	466	22	AA91932	Human reproductive
22	312	9.4	254	22	AA91932	Human protein sequ
23	312	9.4	254	22	AA91932	Human protein sequ
24	286.5	8.6	806	22	AA91932	Human phospholipase
25	284.5	8.5	639	22	AA91932	Human pancreas pho
26	258	7.8	153	22	AA91932	Human human enzyme
27	253	7.6	254	22	AA91932	Novel human enzyme
28	239	7.2	541	22	AA91932	Novel human enzyme
29	238	7.2	237	22	AA91932	Human phospholipase
30	234.5	7.0	332	22	AA91932	Novel human diagno
31	225	6.8	666	22	AA91932	Novel human enzyme
32	175.5	5.3	137	22	AA91932	Novel human enzyme
33	172.5	5.2	102	22	AA91932	Rat phospholipase
34	169	5.1	253	22	AA91932	Novel human enzyme
35	169	5.0	156	22	AA91932	Novel human enzyme
36	168	5.0	240	22	AA91932	Human hCG121 (or C5
37	166.5	4.8	340	22	AA91932	Human hCG121 (or C5
38	160.5	4.8	105	22	AA91932	EGFP-PC-beta fusi
39	144	4.3	918	21	AA91932	Novel polypeptide
40	137.5	4.1	2194	22	AA91932	A novel polypeptide
41	132	4.0	468	21	AA91932	Human Hsgr11 Prote
42	131.5	4.0	468	21	AA91932	Human PRO5990 poly
43	131.5	4.0	468	22	AA91932	Human PRO5990. Ho
44	131.5	4.0	468	22	AA91932	
45	131.5	4.0	468	22	AA91932	

ALIGNMENTS

AA91932 standard; Protein; 561 AA.

ID	AA91932	standard; Protein; 561 AA.
AC	AA91932	
DT	11-DEC-1996	(first entry)
DE	Phosphatidylinositol-4,5-diphosphate specific phospholipase C.	
DE	Phosphatidylinositol-4,5-diphosphate; phospholipase C;	
KW	Columbia ecotype; transformed host; expression vector;	
KW	recombinant production.	
OS	Arabidopsis thaliana.	
XX	Key	Location/Qualifiers
XX	Domain	32..43 "EF Hand"
FT	note=	105..249
FT	Domain	note= "X-domain"
FT	Domain	292..561
FT	Domain	note= "Y-domain"
XX	JP08084585-A.	
XX	02-APR-1996.	
XX	16-SEP-1994;	94JP-0246760.
XX	16-SEP-1994;	94JP-0246760.
XX	(TOYT) TOYOTA JIDOSHA KK.	
XX		

Query Match 21.0%; Score 698.5; DB 22; Length 736;
Best Local Similarity 32.2%; Pred. No. 5e-50;

Matches	192;	Conservative	102;	Mismatches	215;	Indels	87;	Gaps	16;
16	PEQDLVGEVFTIYSENER-MSAEGLLKFLHTEQGDVDFTLDDAKOIMERIR-KDWKKSFG	73							
201	pele---eifhqsgeadvlsapeliefie-dggeeagatlaragqligtvelnetakqhe	256							
74	LASINDLSKEAFKKYIMNDPLNGV--LHNVVHODTQPMWSHVFTTGHNSVLTGNQLSS	131							
257	lmtl-----dgfmmyllspegaaldnthctvcvdmqmpianhyfissshntyltdsqig	310							
132	DSSDTPIAALRRGVVVELDLPDOKGGMKVTHGNTLNPVSFOKCVTAIKNNAFFTSE	191							
311	pssteayvrafagrcrcveidcwegpggepvihgthltskilfrdvqvdrhdaftisp	370							
192	YPCVCTIEDHLSLQGHAAEILEBQILGDALYYPPTDAL-----VEFPSPSLKRKIII	246							
371	YVILSLenhcoglegqqaamarhctilgdm-----vtqaldspnpeelspqqlkgrvli	426							
247	STKPKPEYLEACSTQKLAMENRNILELEKEDKLEQTTFAPLEENHILGENTPSLKEVE	306							
427	k---gkklpaarsedgralsr-----eeeeedeeeee	460							
307	VLSQKEMSTPAELNRSRPSDGEATSTRYSKSNDGNDNPKHFKYARLITIRLAKHAKGTS	366							
461	aaarqlrakispelsalavychat-----rtrthpapa----	496							
367	MEHRLOVDESVKRISLSSEKLEKVVKEWPEALVFRFTOKNLRILVYPAANRVNSNFCPTLA	426							
497	-----pdpqvslserkakkliireagnsfvrhnaqrqltrvyplglrnmnsanyspqem	549							
427	WNYGAQVAQNMGYCKELMQAFKFGKGGGVYLRPOYLLENLPSPGVFNPTSPRNTT	486							
550	wnsgcqlvalnftpgyemdlmagrlfvgngcgyvllkpacrlqdstfapcypgpprtt-	608							
487	LIILKIKVMTLGDWKAFAKRRHDLFSPDPFTFRIVVGVPADEAKWKTS-VVDNSWAPHW	545							
609	--lslqvtlaqlpklnaekphsivdp---lvrieihgvpadcarqetdyvlnngfnprw	663							
546	NEDHEFALCPALALLRIEVRHDDDKDEFFGQGLCPHIEVRDGYRCMOMVYDKKG	601							
664	gqtqlqfqlrapelalvrfvedyatspndfvgqfllpsslkgyrhihllskdg	719							
RESULT	3								
AAAG63220	standard; Protein; 789 AA.								
AAAG63220;									
01-OCT-2001	(first entry)								
Amino acid sequence of a human lipid metabolism enzyme.									
Human; lipid metabolism enzyme; LME; cancer; neurological disorder;									
autoimmune disorder; inflammatory disorder; gastrointestinal disorder;									
cardiovascular disorder; motor neuron disorder; multiple sclerosis;									
demylinating disease; developmental disorder; gene therapy.									
Homo sapiens.									
Key	Location/Qualifiers								
Peptide	1..39								
Modified-site	/note= "signal peptide"								
Modified-site	3								
Modified-site	/note= "potential phosphorylation site"								
Modified-site	37								
Modified-site	/note= "potential phosphorylation site"								
Modified-site	38								
Modified-site	/note= "potential phosphorylation site"								
Modified-site	46								
Modified-site	/note= "potential phosphorylation site"								
Modified-site	115								
Modified-site	/note= "potential phosphorylation site"								
FT	Modified-site	124							
FT	Modified-site	/note=							
FT	Modified-site	129							
FT	Modified-site	/note=							
FT	Modified-site	158							
FT	Modified-site	/note=							
FT	Modified-site	165							
FT	Modified-site	/note=							
FT	Modified-site	169							

CC genetically engineered host cells to express NHP products in vivo. The
CC NHP sequences are useful for generating antibodies, as reagents in
CC diagnostic assays, for identifying other cellular gene products related
CC to NHP and as reagents in assays for screening for compounds that are
CC useful in the treatment of mental, biological or medical disorders and
CC diseases. They can be used to therapeutically augment the efficacy of
CC chemotherapeutic agents used in the treatment of breast or prostate
CC cancer.

XX Sequence 762 AA;

Query Match 20.9%; Score 695; DB 22; Length 762;
Best Local Similarity 32.5%; Pred. No. 1e-49;
Matches 201; Conservative 106; Mismatches 231; Indels 80; Gaps 18;

QY 8 RSTPTKGD-----PRDLVGEVFTIYS-ENERSAEGLLKFLHTEQGDVDFTLDDA 57
Db 186 qsgtlegfevfqykalkraevqelifesadgqkltllefldlqeeqkerdctsla 245
QY 58 KOIMERIRKDWKKSFGSLASINSLSKEAFKYLMPDLNGLVHN-----VHQDMTQPM 113
Db 246 leldryeps-----dsgklrhvlsmdgflsylvcskd--gdifnpacipiyqdmtpqlnh 298
QY 114 YFIFTGHSYLTGNQLSSSSDTPIAAALRGVRVVELDLWPDGKGMKVTGNTLTNPV 173
Db 299 yficsshntylvgdqlcgssvegyiralkrgorcvevdwgdpsgepvvynghttsri 358
QY 174 SFQKVTIAKNNAFFSEYPCVVTIEDHLLTSELOHAAEILQILGDALYPPPTDVAL- 232
Db 359 lfkdvatvayqafqtsdypvvlisethesweqqtmarhlteilgeql-lstldgvlp 417
QY 233 -EPPSPESLKRKIIISTKPKYLEACSTOKLAMENRNLVEELEKEDKLEQTFAPLEEN 291
Db 418 tqpspeelrkilvkgk-----kltleedleyeeceaepeleesela-lesq 464
QY 292 HILGENTPSLRKEVEVLSQKEMSTPAELNSRSPSLDGEATSTRYSKSNDGNDNPKHFKYA 351
Db 465 f-----etepepgeqlnqkdkkkkpkilcpalssivi-----yl 500
QY 352 RLITIRLAKHAGTSMERHLOVDSEVKRISLSKLEKVVKEKPEALVFTQKN---ILR 408
Db 501 kvsfrstfthsk-----ehyhfyeis----sfsetkakrlirk--eagnefvtqhtwqlsr 549
QY 409 VYPAANRVNSNFCPTLAWNGAOMVAONMOGYKELWQAFKFGKNGCGGYVLKPYQLL 468
Db 550 vypsqrldtsdssnyppqelwnagocqmvannmqtaglemidcdghfrqngcgylkpdfir 609
QY 469 ENLPGSVFPNFTSPRNTTLILKIKVMTTLGWDKAFSKRHFDLFSPPDFTRVIVGVPAD 528
Db 610 diqssfhpekpispfkaqtll-iqvisgqqlpkvdktkesivdp---lvkvgifgvrld 665
QY 529 EAKWTSVVDNS-WAPHNEDHEALKCPLEALLRIEVRDHDSDSKDFEGQTCPLTHEV 587
Db 666 targetnyvenngfnpvgqgtcltrvlvpeiamlrfvmvdydksrndfigqytlpwtcm 725
QY 588 RDGYRCMOMYDKKGNVLK 605
Db 726 qggryrhilskdgislr 743

RESULT 5
ABG13669
ID ABG13669 standard; Protein: 787 AA.
XX ABG13669;
AC ABG13669;
XX 18-FEB-2002 (first entry)
DT Novel human diagnostic protein #13660.
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.
XX WO200175067-A2.
XX PD 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US08631.
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX N-PSDB; AAS77856.
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX Claim 20; SEQ ID No 44028; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIP
XX at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 787 AA;

Query Match 19.5%; Score 650.5; DB 22; Length 787;
Best Local Similarity 29.5%; Pred. No. 6.4e-46;
Matches 186; Conservative 107; Mismatches 255; Indels 83; Gaps 15;
QY 28 YSE-NERMSAEGLLKFLHTEQGDVDFTLDDAKQIMERIRKDWKKSFGSLASINSLSKEAF 86
Db 9 ysdkdhltveelaqlfkveqkmnnvtdtclidkikfevseen-----kvknvlgtegf 63
QY 87 RYLMNP--DLNGLVHNVVHODMTQPMSHYFIPTGHSYLTGNQLSSSDSTPTAAALRR 144
Db 64 tnmrspacdifnplhhevyqmdqplcnvnyasshntytgtdqlsqskvdmayarvlqe 123
QY 145 GVRVVELDLWPDGKGMKVTGNTLTNPVSPQKCVTAIKNNAFFTSEYPCVVTIEDHLTS 204
Db 124 gcrvevdcdwdpdpgepvvhgtyltskllfrvvetinkhafvknepfvilsienhcsi 183
QY 205 ELQGHAAEILEQILGDALYPPPT-TDALVEFPSPESLKRKIIISTKPKYLEACSTOKL 263
Db 184 qqqrkiagylkgifgdikldssvdtgeckqlpspqskgkilkvkgklpyhnl-gddaeg 242
QY 264 AMENRNLVEELEKEDKLEQTFAPLEENHILGENTPSLRKEVE-VLSQKEMSTPAELNSR 322

Db 243 evsdsadsadeckfklhysngtthqv-----esfirkklesllkesqirdekdpdsf 298
 QY 323 SPDLGEAT-----STRYSKSDNGNDNPKFKYARLITIRLAKHAGT---SMEHRLQVDE 375
 Db 299 tvrallkatheglnahlikgdpdkesgk-shgrslmtngfghkhtkrsksystdddee 357
 QY 376 SVKR-----ISLSESK 386
 Db 358 dtqgstqkeggqlylgrrrrktmkclrelsdlyvvtnsvaadqdivdgttgnvlsfsetr 417
 QY 387 LEKVEKWPALVKFTQKNILRYVPAANRVNSNFCTPLAWNYGQMAVQMGYKELW 446
 Db 418 ahgvvqkseqfmlyngkqlitriypsayridsnfnplwynagcqlvalnvgsegrmmq 477
 QY 447 QAGKFKNGCGGVYLPQVLLNLSGVPFNPPTS-----PRNTTLIKIKVMTTLGWOKA 502
 Db 478 lnrakfkangncvylkpgcmckg-----tfnpfsgdplpanpkkqlilkvisgqqlpkp 532
 QY 503 FSKRHFDLFPDPFFFTFRTVIVGVGPADEAKWKTSVV-DNSWAPHWNEDHEFALKCPDELALL 561
 Db 533 pdsfmfdrgelidpfveveileglpvdccdkdqrtrvddngfnpvweetitftvhppeialv 592
 QY 562 RIEVRHDDSDKDEFEQTCPLPIHEVRDGYR 592
 Db 593 rflvwdhdpigrd-fvgqtrvtvsslvpgyr 622

RESULT 6

AAW81394

ID AAY81394 standard; protein; 756 AA.

AC AAY81394;

DT 19-JUN-2000 (first entry)

DE Rat phospholipase C-delta-1.

XX

KW Phospholipase C-delta-1; rat; PH domain; inositol triphosphate;
 KW quantitation; distribution; fluorescent label; hypertension;
 KW inflammation; dementia; immunodeficiency; diagnosis; treatment.

OS Rattus sp.

XX

FH Key

FT Domain

Location/Qualifiers

1..147

/note= "PH domain"

XX WO200011213-Al.

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CC quantitating inositol triphosphate concentration and determining the
 CC distribution of inositol triphosphate in cells using the fluorescent
 CC probe. The fluorescent phospholipase C-delta probes of the invention may
 CC be used for simple and accurate quantitation of inositol triphosphate and
 CC its distribution in cells. It is also useful in the diagnosis and
 CC treatment of hypertension, dementia, inflammation and immunodeficiency,
 CC as well as in drug development. The present sequence represents rat
 CC phospholipase C-delta-1.
 XX
 SQ Sequence 756 AA;

Query Match 17.9%; Score 594.5; DB 21; Length 756;
 Best Local Similarity 28.7%; Pred. No. 3.3e-41;
 Matches 173; Conservative 96; Mismatches 215; Indels 119; Gaps 16;

QY 32 ERMSAGSLKFLHTEGGVDFTLDQAKQIMERIRKDWKSKFGLASINDLSKEAFKRYLM 91
 Db 226 etlsverlvtfiqhgreeeagpalalslieryeps-----etakaqrmtkdgflmyli 280
 QY 92 NPDLN--GVLHNHVHODMTOPMSHYFIFTGHSNYLTGNQLSSDSDTPIAAALRRGVVV 149
 Db 281 sadgnafslahrsvyqmdqpsihylvssshntylledqtlgtspsteayiralcgcrcl 340
 QY 150 ELDLWDDPDKGGMKVTHTNTLTNPVSFQKCVTAIKNNAFTSEYPCVVTIEDHLTSELQGH 209
 Db 341 eldcwdgpnqepiivhytftskilfcvldiradyafkaspyvllslenhcsleqgrv 400
 QY 210 AAEILEQILGDALYPTTDLVPEPPSPESLKRKIIISTK-----PPK 252
 Db 401 marhlrailgplldqpldgvttslpspeqlkgkllkgkllgllpaggengseatdvs 460
 QY 253 EYLEACSTQKLAENNRNLVEELEKEDKLEQTFAPLENNHILGENTPSLKEVEVLSQKE 312
 Db 461 deveaaamedeav--rsqvqhkpkedkl-----vpe----- 492
 QY 313 MTPAELNSRSPDLSGEATSTRYSKSDNGNDNPKHFKYARLITIRLAKHAKGTSMEHRLQ 372
 Db 493 -----sdm-----liycks-----vhfg-----gfsspglsgqafye 519
 QY 373 VDESVKRISLSSEKLEKVEKPEALVKFTQKNILRYVPAANRVNSNFCTPLAWNYGAO 432
 Db 520 m-----asfsearalrllgesngfvrhvnvscslriypagwrtsdnsyspvmwngq 573
 QY 433 MYAQNMQYKELWQAFKFGNGCGGVYLPQVLLNLSGVPFNPPTSPTNTTLI----- 488
 Db 574 ivalnfqtpgemdyllgcfdnggcgyvikpafld-----pntfnsraitqgp 624
 QY 489 -----LKIVMTTLGWDAFSAKRHFDLFPDPFFFTFRTVIVV--GVPADEAKWKTSVV-DN 539
 Db 625 wrperlrviisgqqlpkv-nknksivdp-----kvivehlgvgrdtgsrtavltinn 678
 QY 540 SWAPHWNEDHEFALKCPDELALLRIEVRHDDSDKDEFEQTCPLPIHEVRDGYRCHQWMDK 599
 Db 679 gfnprwmeleftevtvpdlalvrmvedydskskndfkggstipwnslkqgyrhvhlisk 738
 QY 600 KGN 602
 Db 739 ngd 741

RESULT 7

AAW01596

ID AAW01596 standard; Protein; 1096 AA.

XX AAW01596;

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17-MAR-1997 (first entry)

Inositol-1,4,5-triphosphate binding protein.

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Claim 11; Page 14-18; 22pp; Japanese.
 The invention relates to a fluorescent probe comprising phospholipase
 C-delta (or a portion thereof, such as the PH domain) and a fluorescent
 substance. The invention also encompasses fusion genes encoding a fusion
 protein of phospholipase C-delta (or a portion thereof) and a fluorescent
 protein (e.g. green fluorescent protein, GFP) and methods for

Query Match	16.4%;	Score 545.5;	DB 22;	Length 677;
Best Local Similarity	29.4%;	Pred. No. 3.9e-37;		
Matches 159;	Conservative 81;	Mismatches 206;	Indels 95;	Gaps
QY	89	YLMNPDLNGVLNVVHODMTQPMASHYFTFTGHNSLYLTGNOLSSDSDTPIAAALRRGVKV	148	
Db	6	yifde-----hkkvcqdmkqplshyfinsshtylliedqfrgsdityiralkmgrs	60	
QY	149	VELDLDPDGGKMKVTHGNTLNPVSFOKCVTALKNNAPFTSEPVYCVVIEDHLTSELQ	208	
Db	61	veldvwdgpdneplytghtmtsqtivrsvidinkiyaffaseypliliclenhcsikgqk	120	
QY	209	HAAEILEOILGALYPPPTDALVE---FFSPSLKRKIIISTKPPKPEYLEACSTQKILAM	265	
Db	121	vmvqmkkilgdkly---ttspnveesylpspdvlgkllikakk-----	162	
QY	266	ENRNLVEELEKEDKLEQTFAPLEENHILGENTPSLRKEVEVLSQEMSTPAELNSRSPS	325	
Db	163	-----lssncsgvegdv-----lssncsgvegdv-----tde	177	
QY	326	DLGEATSTRYSKSN--DGNDNP-KHFKYARLIT--IRLAKHAKGTSMEHLRQVDSEVKRI	380	
Db	178	degaemsqrmdekemegpnvnpkrifqlckeliselvsicksvqfkefqsvfqkywevc	237	
QY	381	SLSESKLEKVVYKWEALVKFTQKILNLRVYPAANRVNSNFCPTLANNYGAQVQAQNMQG	440	
Db	238	sfevelaskyanenpgdfvnyvnrflarfpspmridsnnmpdqfkwccqivamnfqt	297	
QY	441	YKELIWAQAFGRKNGCGVVLKPOVLLB-----NLPSPGVNPNTSPRNTTLILKIKV	493	
Db	298	pglmldnigwfrqngcngyvirpaimreevsffsantkdsvp--gvspq---llhiki	351	
QY	494	MTILGNWK-AFSRHRHDLFSPDPDFTRVIVGVPADEAKWKTIV--DNSWAPHWNEDHEF	551	
Db	352	isgnfipkpgsgakgddvdp---yyvveihgipadcaeqrtktvhngdapiidesfef	408	
QY	552	ALKCPALALLRIEVRDHDDSDKDEFEGOTCLPIHEVRDGYRCHQMVDKKGNVLKGLMLF	611	
Db	409	qinipelamrvfvld-dyigidefigdytipfecldqgrhryplsgltgewlahasifv	467	
QY	612	H 612		
Db	468	h 468		
RESULT	9			
ID	AAG25435			
XX	AAG25435 standard; Protein; 217 AA.			
AC	AAG25435;			
XX				
DT	17-OCT-2000 (first entry)			
XX				
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 29498.			
XX				
KW	Protein identification; signal transduction pathway; metabolic pathway;			
KW	hybridisation assay; genetic mapping; gene expression control; promoter;			
KW	termination sequence.			
XX				
OS	Arabidopsis thaliana.			
XX				
PN	EP1033405-A2.			
XX				
XX	06-SEP-2000.			
XX				
PF	25-FEB-2000; 2000EP-0301439.			
XX				
PR	25-FEB-1999; 99US-0121825.			
PR	05-MAR-1999; 99US-0123180.			

PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145218.
PR 26-JUL-1999; 99US-0145224.
PR 27-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 28-JUL-1999; 99US-0145919.
PR 02-AUG-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0146389.
PR 04-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 10-AUG-1999; 99US-0147935.
PR 11-AUG-1999; 99US-0148171.
PR 12-AUG-1999; 99US-0148319.
PR 13-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 16-AUG-1999; 99US-0148684.
PR 17-AUG-1999; 99US-0149368.
PR 18-AUG-1999; 99US-0149175.
PR 20-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 23-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 25-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150366.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151080.
PR 31-AUG-1999; 99US-0151303.
PR 01-SEP-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 10-SEP-1999; 99US-0152363.
PR 13-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 16-SEP-1999; 99US-0154018.
PR 20-SEP-1999; 99US-0154039.
PR 22-SEP-1999; 99US-0154779.
PR 23-SEP-1999; 99US-0155139.
PR 24-SEP-1999; 99US-0155486.
PR 28-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.

PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0158369.
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PR 26-OCT-1999; 99US-0161359.
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PR 26-OCT-1999; 99US-0161360.
PR 28-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 28-OCT-1999; 99US-0162142.

Query Match

Best Local Similarity 16.3%; Score 543; DB 21; Length 217;
Matches 103; Conservative 33; Mismatches 71; Indels 4; Gaps 2;

QY 399 VKTQKNILRYVPAANRVSSNFCPTLAWNYGAOMVQYKELWQAFKFGNGGC 458
Db 6 vrtqgnliriykgrvtvssnynplvgwshgqmvafnmqgygrslwlmqgmfranggc 65
QY 459 GYVLKPYLLENLPSCVPFNP--TSPRNTTLIKYKVTTLGNDKAFSKRHFDFSPDF 516
Db 66 gyikpdlilksgdsdldfipkvtkt--lrvtymgegywfydfrthtdgyspdf 123
QY 517 FTRVIVGVPADEAKWTSVDNSWAPHNEDHEFALKCPDLALLRIEVRDHDSDKDF 576
Db 124 ytrvgiagvpgdtvmkktlednwipawdevfeftvpepallrlievheydmsekddf 183
QY 577 EGQTCLPIHEVRDGYRCMQYDKGNVLKV 607
Db 184 gqgtclpweisegirafplhsrkgekykv 214

RESULT 10

AAE13101
ID AAE13101 standard; Protein; 1809 AA.
XX
AC AAE13101;
XX

DT 28-JAN-2002 (first entry)

DE Human phospholipase C family member, 16836 protein.

KW Human; phospholipase C; PLC; 16836 protein; cellular disorder; sarcoma;
KW carcinoma; metastatic disorder; leukaemia; bone disorder; osteoporosis;
KW haematopoietic neoplastic disorder; sarcoidosis; Alzheimer's disease;
KW Parkinson's disease; brain disorder; reproductive disorder; gonorrhoea;
KW teratoma; immune disorder; rheumatoid arthritis; cardiovascular disorder;
KW Grave's disease; atherosclerosis; cardiomyopathy; anorexia nervosa;
KW obesity; cachexia; lipid disorder; diabetes; hepatocellular cancer;
KW viral disease; gene therapy; cytostatic; osteopathic; immunosuppressive;
KW neuroprotective; dermatological; ophthalmological; nontropic; vasotropic;

Sun Jul 28 10:34:35 2002

KW hypotensive; anticonvulsant; antibacterial; tuberculostatic; virucide;
XX vulnerary; anorectic.
OS Homo sapiens.

XX Location/Qualifiers
XX 35..338
XX /label= RasGEF domain
XX /note= "Ras guanine nucleotide exchange factor domain"
XX 900..1048
XX /label= PI-PLC-X domain
XX /note= "Phosphatidylinositol-specific
XX phospholipase C-X domain"
XX 1171..1184
XX /label= PI-PLC-Y domain
XX /note= "Phosphatidylinositol-specific
XX phospholipase C-Y domain"
XX 1261..1353
XX /label= PI-PLC-Z domain
XX /note= "Phosphatidylinositol-specific
XX phospholipase C-Z domain"
XX 1378..1460
XX /label= C2 domain
XX 1640..1745
XX /label= RA domain
XX /note= "Ras association domain"

XX WO200175121-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US10273.
XX 31-MAR-2000; 2000US-193921P.
XX (MILL-) MILLENNIUM PHARM INC.
XX Meyers RA, Hunter JJ;
XX WPI: 2001-662975/76.
XX N-PSDB; AAD21290.
XX New polypeptide for controlling cellular proliferative and/or
XX differentiative disorders such as lung, breast or colon cancers,
XX comprises a member of human phospholipase C family, referred to as
XX 16836 -

XX Claim 9; Fig 1; 148pp; English.
XX The present invention relates to novel human phospholipase C (PLC)
XX family members, designated as 16836 and polynucleotides encoding
XX them. 16836 sequences are useful for treating cellular proliferative
XX and/or differentiative disorders such as carcinoma, sarcoma, metastatic
XX disorders or haematopoietic neoplastic disorders (e.g. leukaemias)
XX which arise from myeloid, lymphoid or erythroid lineages or their
XX precursor cells. They are also useful for treating bone disorders
XX (e.g. osteoporosis, sarcoidosis), brain disorders (e.g. Alzheimer's
XX disease, Parkinson's disease), reproductive disorders (e.g. gonorrhoea,
XX teratoma), immune disorders (e.g. rheumatoid arthritis, Grave's disease),
XX cardiovascular disorders (atherosclerosis, cardiomyopathies) or diseases
XX of metabolic imbalance such as obesity, anorexia nervosa, cachexia,
XX lipid disorders and diabetes. 16836 molecules of the invention are
XX used to treat disorders associated with an accumulation in the liver
XX of fibrous tissue, such as that resulting from an imbalance in the
XX production and degradation of the extracellular matrix accompanied
XX by the collapse and condensation of preexisting fibers. They are
XX useful as markers for precursors or predisposition of disorders
XX or disease states, as markers of drug activity or as markers of the
XX pharmacogenomic profile of a subject. Modulators of 16836 activity
XX could be used to control viral diseases. They are used in the treatment
XX and/or diagnosis of virus-associated carcinoma, especially hepatocellular
XX cancer. 16836 sequences are also used in gene therapy. The present
XX sequence is phospholipase C (PLC) family member, 16836 protein from

CC human.
XX Sequence 1809 AA;
SQ

Query Match 15.3%; Score 508.5; DB 22; Length 1809;
Best Local Similarity 24.1%; Pred. No. 2.5e-33;
Matches 167; Conservative 121; Mismatches 240; Indels 165; Gaps 21;
QY 38 GLLK---ELHTEQGVDFLDDAKQIMERIKDKWKSFGSLASINSLSKAEAFKRYLMNPD 94
DB 832 gilqlndflvncqge-hctydeillsiqk-----fepsismch-qgllmsfegfarflmdc 885
QY 95 LNVGLHNVVHQ---DMTQPMNSHYFIFTGNSYLTQNLSSDSDPTPIAALRRGVVVE 150
DB 886 -afskndesqenikelplisyvyyesshntyltghlkgesvvelyqvllqgrsv 944
QY 151 LDLPDDKGMKVTGNLTNPVSFOKVTAKNNAPFTSEYPCVCTIEDHTTSELQHA 210
DB 945 ldcwdgdgmpliyhgtlttkipfkveveaidsafinsdplliisienhcselpqgrkm 1004
QY 211 AEILEOILGDALYPPPTDVALVE-----FSPESLKRKIIISTK-----PPREYLE 256
DB 1005 aelfktvfgekl---vtklfetsddpmlpspdqrlrkvlknkklkahqtpvdlk 1060
QY 257 ACSTQKLAMENR-----NLVELEKEDKLEQTTFAPLEENHILGENTP----- 299
DB 1061 qkahlasmqvgayngnanpranneeedeedy-dyeslsddnil-edrpenksc 1118
QY 300 -----SLRKEVEVLSQKEMSTPAELNSRSPDGLGEATSTRYSKSNQNDNP----- 345
DB 1119 ndklqfeyneeipkrirkkadsnckgkydmeelgeefyldqnkkesqlapelsdiv 1178
QY 346 -KHFYARLITIRLAKHAKGTSMEHRLQV-----SLESKLEKVKWPEALVKFTOKNILRVYPA 413
DB 1179 eqavkfpglscinasgsrgerksrksifgnnpgrmspgetasfnktsgksscegirqt 1238
QY 374 -DESVKRI-----SLESKLEKVKWPEALVKFTOKNILRVYPA 413
DB 1239 weessspnpttsisairtpkcyhisslnenaakrlcrrysqkltqhtacqllrtypaa 1298
QY 414 NRVNSNCPCLTANNYGAVQAMQNGYKELMQAFKFGKNGCGYVLLKPOYLLE-NLP 472
DB 1299 tridsnnpnplmfwhglqlvalnyqlddlplhlnaamfeangcgvykppvldkncp 1358
QY 473 SGVPNPSPRNTLILKIKVMTLGDWDAFSGRHFDFLSPDFPFFTRVI----- 521
DB 1359 myqkfspL-----erldsmdpavysltivsggnvcpnsnm 1394
QY 522 -----VVGVPADAEAKWKTSSVD-NSWAPHNEDHEFALKCPELALLRIEVRDHD 572
DB 1395 gspcievdivgmpldschfrtkphrntlnpmwneqflhvfhdvlfvavvennsa 1454
QY 573 KDEFEQGTCLPHEVRDGRCHQMVDKKGNVLK 605
DB 1455 ---vtadriiplkalkrgyrhqlrnlhnevie 1484
RESULT 11
ID AAM80177 standard; Protein; 1058 AA.
XX AAM80177;
XX AC AAM80177;
XX DT 06-NOV-2001 (first entry)
XX DE Human protein SEQ ID NO 3823.
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX KW tissue growth factor; immunomodulatory; cancer; leukaemia;
XX KW nervous system disorder; arthritis; inflammation.


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PR 23-MAR-2000; 2000US-0614150.
PR 11-JUL-2000; 2000US-0614150.
PA (PEKE ) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI: 2001-656860/75.
XX N-PSDB; ABL04858.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions
XX
XX Disclosure; SEQ ID NO 9057; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutic and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), the encoded proteins
XX (AB57737-AB572073).
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
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XX Sequence 1312 AA;
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XX Query Match 14.08; Score 464.5; DB 22; Length 1312;
XX Best Local Similarity 25.58; Pred. NO. 8e-30;
XX Matches 178; Conservative
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XX 9 SCTPGDPEQDLVG-----EVFTIY-----SENER-----MSAEGLLKFLH 44
XX 193 tglpsgkvdsivskfgedfylnlylqtqrseverlfdsvgnskrkcmiaqlvefin 252
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XX 45 TEOGD-----VDFTLDDAKQIMRIRKDKWKKSGFLASINSDLSEAFKRYLMPDUNGVL 99
XX 253 ktdrprlneiipypanparakellqyepnkfn--aqqgklsigdlgrlymgdd-nplm 309
XX 100 HNV---VHQDMPQMSHVFIETGNSVLTGNQLSSDSDPTAAALRGVRVWELDLWPD 156
XX 310 apskldldcdmdpmshyafinshtytlgqltgkssveilyrqclagrcvelfwng 369
XX 157 DRGGMKVTHGNLTNPVFSFOCKVATKNNAFFTSEYPCVTIEDHTTSELGHAAIELEQ 216
XX 370 rteepvvhvyfypelfafkdviaeafktseypvillsfenhcnprqakianycre 429
XX 217 ILGDALYVPP-----TTDALVEFPPESELRKKIIITKPKPEV-----254
XX 430 ifgdmldkpldshlepnmdlppamllrrkilkknkhhhhhhhhhhhhhhhhhhhhhhhh 489
XX 255 -----LEAGSTOKLAM-----ENRNLVEELEKEDKLEQTFFA-----PLE--289
XX 490 nkhltansvdakaagvgisashedgvgtrstangdvagtgagtaghnaplqlqi 549
XX 290 -----ENHILGENTPSLRKEVE-----VLSOKEMSTPAELNRSRPSDLGE 329
XX 550 rqsksdstgssdsdsedeslptnptlpsgnepppekaqketeagaeiaa: 601
XX 330 ATSTRYSKSDGNDNPKHFKYARLITRLAKHAKGTSMERHLOVDSEVKRITSSESLEKX 389
XX 602 -lrvnyvq-----pihf-----ssfenaeknrcyemssfdkqatt 636
XX 390 vvekwpealvktoknlrlrvypanrsvnsfctplawnygaqmwqonmqgygkclwqaf 449
XX 637 lkerpiefvnynkhlisrvypagtrfdsnfmplfwagcqlvalnftldamqln1 696
XX 450 GKEFGNGGCGYVLYKPOYLLENLPISGVFPNTPSPRNTTILKIKYMTLIGWDKAFSRHED 509
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us-09-828-447-12.rag

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Db 697 gifeynarsgylkpefmrdsrldpfaestvdg--iaagtvtlsgqfildkr-- 751
QY 510 LFSPPDFTTRVIVGVGVPAD--BAKWKTSV--DNSWAPHNNEDEHFAK--CPELALIRI 563
Db 752 ----antfvevdmglpadtrvkkfrktvrdngmmplydee-pfvfkkvlpeliasiri 806
QY 564 EVRDHDDSKDEFEGQTCPLPIHEVRDGYRCYRCOMYDKKG 601
Db 807 aa--yeeggk-lghrvlpvlgpcpgyrvhnrisevg 840

RESULT 15
AAG25436
ID AAG25436 standard; Protein: 178 AA.
AC AAG25436;
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XX 17-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 29499.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 16-APR-1999; 99US-0128714.
PR 19-APR-1999; 99US-0128845.
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PR 02-AUG-1999; 99US-0146386.
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PR 03-AUG-1999; 99US-0146389.
PR 04-AUG-1999; 99US-0147038.
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PR 05-AUG-1999; 99US-0147192.
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PR 09-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.

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PR 09-AUG-1999; 990S-0147935.
PR 10-AUG-1999; 990S-0148171.
PR 11-AUG-1999; 990S-0148319.
PR 12-AUG-1999; 990S-0148341.
PR 13-AUG-1999; 990S-0148565.
PR 13-AUG-1999; 990S-0148684.
PR 16-AUG-1999; 990S-0149368.
PR 17-AUG-1999; 990S-0149375.
PR 18-AUG-1999; 990S-0149426.
PR 20-AUG-1999; 990S-0149722.
PR 20-AUG-1999; 990S-0149723.
PR 20-AUG-1999; 990S-0149929.
PR 23-AUG-1999; 990S-0149902.
PR 23-AUG-1999; 990S-0149930.
PR 25-AUG-1999; 990S-0150566.
PR 26-AUG-1999; 990S-0150884.
PR 27-AUG-1999; 990S-0151065.
PR 27-AUG-1999; 990S-0151066.
PR 27-AUG-1999; 990S-0151080.
PR 30-AUG-1999; 990S-0151303.
PR 31-AUG-1999; 990S-0151438.
PR 01-SEP-1999; 990S-0151930.
PR 07-SEP-1999; 990S-0152363.
PR 10-SEP-1999; 990S-0153070.
PR 13-SEP-1999; 990S-0153758.
PR 15-SEP-1999; 990S-0154018.
PR 16-SEP-1999; 990S-0154039.
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PR 24-SEP-1999; 990S-0155659.
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PR 04-OCT-1999; 990S-0157117.
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PR 22-OCT-1999; 990S-0160980.
PR 22-OCT-1999; 990S-0160981.
PR 22-OCT-1999; 990S-0160989.
PR 25-OCT-1999; 990S-0161404.
PR 25-OCT-1999; 990S-0161405.
PR 25-OCT-1999; 990S-0161406.
PR 26-OCT-1999; 990S-0161359.
PR 26-OCT-1999; 990S-0161360.
PR 26-OCT-1999; 990S-0161361.
PR 28-OCT-1999; 990S-0161920.
PR 28-OCT-1999; 990S-0161922.
PR 28-OCT-1999; 990S-0161993.
PR 29-OCT-1999; 990S-0162142.

Query Match 12.9%; Score 430; DB 21; Length 178;

Best Local Similarity 47.5%; Pred No. 3e-28;
Matches 84; Conservative 26; Mismatches 63; Indels 4; Gaps 2;

QY 433 MVAQNMQYGGKELMQAFKKGCGGYVLPQYLLLENLPSCGFNP--TSPRNTTLIK 490

Db 1 mvafnmgygrslwlmggmfranggcgyikkpdlillksdsdldfdpkatlpvkt--lr 58
QY 491 IKVMTTLGWDKAFSKRHFDLFSPPDFFTRVIVGVPADEAKWKTSVVDNSWAPHWEDHE 550
Db 59 vtvymgegwyfdfrhthfdgysppdytrvgiagvpdgtvmkkctktledhwpawdevfe 118
QY 551 FALKCPALALRIEVRDHDSDKDEFEQGTCLPIHEVRDGYRCMQMYDKRGKGNVLKV 607
Db 119 fpltvpelallrlvheymsekddfggtclpwwelsegirafplhbrkgekyksv 175

Search completed: July 26, 2002, 17:23:18
Job time: 4641 sec

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3	123.5	3.7	573	4	US-08-235-836C-112	Sequence 112, Appli	
4	120	3.6	2482	1	US-08-328-254-6	Sequence 6, Appli	
5	120	3.6	3248	1	US-08-353-700-1	Sequence 1, Appli	
6	120	3.6	3248	5	PCT-US95-16216-1	Sequence 1, Appli	
7	115	3.5	904	4	US-09-198-484-2	Sequence 2, Appli	
8	113.5	3.4	834	1	US-07-977-434-8	Sequence 8, Appli	
9	113.5	3.4	834	1	US-08-458-819-8	Sequence 8, Appli	
10	113.5	3.4	834	5	PCT-US91-07035-8	Sequence 8, Appli	
11	107	3.2	640	3	US-09-026-343-2	Sequence 2, Appli	
12	104.5	3.1	834	1	US-07-977-433-2	Sequence 2, Appli	
13	104.5	3.1	834	1	US-08-073-384C-6	Sequence 10, Appli	
14	104.5	3.1	834	1	US-08-254-359A-6	Sequence 6, Appli	
15	104.5	3.1	834	1	US-08-384-490-31	Sequence 6, Appli	
16	104.5	3.1	834	1	US-08-483-043-6	Sequence 31, Appli	
17	104.5	3.1	834	1	US-08-459-383-31	Sequence 6, Appli	
18	104.5	3.1	834	1	US-08-458-813-10	Sequence 31, Appli	
19	104.5	3.1	834	1	US-08-481-238-6	Sequence 10, Appli	
20	104.5	3.1	834	2	US-08-471-066B-6	Sequence 6, Appli	
21	104.5	3.1	834	2	US-08-484-956-6	Sequence 6, Appli	
22	104.5	3.1	834	2	US-08-757-653-6	Sequence 6, Appli	
23	104.5	3.1	834	2	US-08-599-491-6	Sequence 6, Appli	
24	104.5	3.1	834	2	US-08-756-386-6	Sequence 6, Appli	
25	104.5	3.1	834	2	US-08-823-516-6	Sequence 6, Appli	
26	104.5	3.1	834	3	US-08-682-853A-6	Sequence 6, Appli	
27	104.5	3.1	834	3	US-08-753-038-6	Sequence 6, Appli	

us-09-828-447-12.ra1

Sun Jul 28 10:34:35 2002

APPLICANT: MACLEOD, ANGUS M.
 APPLICANT: MERCHANT, KEVIN J.
 TITLE OF INVENTION: INHIBITORS OF PHOSPHOINOSITIDE-SPECIFIC
 TITLE OF INVENTION: PHOSPHOLIPASE C
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSES: DAVID A. MUTHARD
 STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
 CITY: RAHWAY
 STATE: NEW JERSEY
 COUNTRY: U.S.A.
 ZIP: 07065

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/138,133
 FILING DATE:

CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: MUTHARD, DAVID A.
 REGISTRATION NUMBER: 35,297
 REFERENCE/DOCKET NUMBER: 18938
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-3903
 TELEFAX: (908) 594-4720
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1290 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-138-133-2

Query Match 12.3%; Score 409.5; DB 1; Length 1290;
 Best Local Similarity 20.0%; Pred. No. 5.6e-27;
 Matches 194; Conservative 88; Mismatches 252; Indels 437; Gaps 26;

QY 78 NSDLSKEAFKYLMPDNLGVHNVHDMTPQMSHYFTFTGHSNLTGNQLSSDSTP 137
 Db 303 ---FSKE-----NSVNSQLDVCPEPMNPLSHYSSHTYLTGDFSSSESSLEA 352
 QY 138 IAAALRRGVVVELDLWPDGKGMKVTGNTLTNPVSFKCVTAIKNNAFFTSYPCVVT 197
 Db 353 YARCLRMGRCIELDCWDGPMVYIHTGHTLTTKIKESDVLHTIKHAFVASEYPVLS 412
 QY 198 IEDHLSLQGHAAEILQILGALYPTTDLVPEPSPESLKRKIIISTK----- 249
 Db 413 IEDHCSIAQORNAQHFRKVLGDTLLTKPVDIAADGLSPNQLKRLIKHKKLAEGSAY 472,
 QY 250 ----- 249
 Db 473 EEVPTSMYSENDISNKGILYLEDVNVHWPVHYFVLTSSKIYSEETSSDQNEDE 532
 QY 250 -PKE---YLEACSTOK-----LAMENRNILVEELEKEDKLE-----OTTFALEENHIL 294
 Db 533 EEPKASGSELHSSSEKWFHGLGAGRGHIAERLLTEYCIETGAPDGSFLVRESETFV 592
 QY 295 GENTPSLRKEVEVL-----SOKEMSTP----- 316
 Db 593 GDYTLSEWRNGKQVHCRIHSRQDAGTPKFFLTDLNVLVFDLSLYLTHYQVPLRCNEFEMR 652
 QY 317 -----AELNSRSPDLGEATSTR-----YSKNDGND----- 343
 Db 653 LSEVPQTNHESKEWTHASLTRAQAEHMLMRVPRDGAFLVRKRNEPNSYAFRAEGKI 712
 QY 344 ----- 343
 Db 713 KHCVRVQGGVQVMLGNSEFSLVDLSYVEKHPYKMKLRYPINEAEKIGTAEPDYG 772
 QY 344 -----NPKHF----- 348
 Db 773 ALYEGRNPGFVEANPMTFCAVKALFDYKAQREDELFTKSAIQNVKODGGWGRGD 832
 QY 349 -----KYA 351
 Db 833 YGKKQLMFPNSYVEEMINPAILEPEREHLDENSPLGLDGLLVDPACQIAIRPEGKNN 892
 QY 352 RLITIRL-----AKHAKGTSMEHR-----LO 372
 Db 893 RLFEVSIEMPSVAQSLDVAADSOEQLDWWKIREVAQTAARLLEGKMERKRIKALE 952
 QY 373 VDES-----KRI-----SLSEKLEKVEKWEALVFETOKNIL---R 408
 Db 953 LSELVYVCRPVDFDEKIGTERACRYRDMSEFPETKAEKYNNKAKGK--KFLQVNRQLSR 1010
 QY 409 VYPAANRVNSNFCPTLAWNTGAQVVAQNMGGYKELWQAFGFKGNGGGYVYLPQYLL 468
 Db 1011 IYKQRLDSSNVYDPLPMWICGSQLVALNFQTPDKPMQNALFMAGHGGYVLPQSTWR 1070
 QY 469 ENLPSPVNPSPRN--TTLILIKVMTTLGWDKAFSKRHFDFLSPDPDFTRVIVGVPA 527
 Db 1071 DE--AFDPDKSLRGLEPCVICIEVGA---RHLKNGRGIVCP---FVEIEVAGAEY 1121
 QY 528 DEAKWITS--VDNSWAPHW--NEDHEFALKCPCLALLREVDHDDSKDFEGGTCLPIH 585
 Db 1122 DSTQKTEFVDNGLNVPVPAKPFHQISNPEFAPLFVYVEEDMFSDQNFQAQATFPVK 1181
 QY 586 EVRDGYRCMQM 596
 Db 1182 GLKGTGYRAVPL 1192

RESULT 2
 US-08-138-133-2
 ; Sequence 2, Application US/08138133
 ; Patent No. 5519163
 ; GENERAL INFORMATION:
 ; APPLICANT: GIBBS, JACKSON B.
 ; APPLICANT: KOBLAN, KENNETH S.

QY 344 ----- 343
Db 713 KHCVRQEGQTVMLGNSEFSLVDLSIYERHPLRYKMKLRYPINEEALEKIGTAEPDYG 772
QY 344 -----NPKHF----- 348
Db 773 ALYEGRNGFYVEANPMPTFKCAVKALFDYKAQREDELFTTKSAIONVEKODGQWGRGD 832
QY 349 -----KYA 351
Db 833 YGKKQLWFPNSYVEEMINPAILEPEREHLDENSPLGLLRGLVDVPACQAIAPRKGNN 892
QY 352 RLITIRL-----AKHAGTSMHR-----LQ 372
Db 893 RLFFVESISMPVAQNSLDVAADSQEQLDWYKKIREVAQTADARLITECKMMERRKKIALE 952
QY 373 VDESV-----KRI-----SLESKEKVKVWPALVKFTQKNIL-----R 408
Db 953 LSELVYCRPVDFDEKIGITERACRYRDMSSFPETRAEYVNAKAGK--KFLQYNRLQLSR 1010
QY 409 VYPAANRVNSSFNFCPTLAWNTGAOMVONMOGYGKELWQAFGKNGCGCYVLKPOVLL 468
Db 1011 IYPKGORDSSNYDPLPMWICSGVLVNFQPDPMQMNQALFMAGHGCGYVLOPSTMR 1070
QY 469 ENLPSGVFPNTPSPRN--TTLILKIKVMTTLGWDAFASRRHFDLFSPPDFTRVIVGVPA 527
Db 1071 DE--AFDPFKSLRGLRGLPCVICIEVGA----RHLPKNGRGI--FVEIEVAGAEY 1121
QY 528 DEAKWKT--VVDNSWAPIW--NEDHEFALKCPDELALLRTEVRDHDSDKDEFEGETCLPIH 585
Db 1122 DSTKOTKEFVVDNGLNVPWPAKPFHQISNPEFAPLFRVYVEEDMFSDQNLQAQATFVK 1181
QY 586 EVRDGVCRCMQM 596
Db 1182 GLKGTIRAVPL 1192

RESULT 3

US-08-235-836C-112
; Sequence 112, Application US/08235836C
; Patent No. 6248562
; GENERAL INFORMATION:
; APPLICANT: Dunn, John J.
; APPLICANT: Luft, Benjamin J.
; TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
; TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brookhaven National Laboratory
; STREET:
; CITY: Upton
; STATE: NY
; COUNTRY: USA
; ZIP: 11973
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,836C
; FILING DATE: 29-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,191
; FILING DATE: 01-11-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Bogosian, Margaret C.
; REGISTRATION NUMBER: 25,324
; REFERENCE/DOCKET NUMBER: BNL93-28A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 282-7338

; TELEFAX: (516) 282-3729
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-235-836C-112

Query Match 3.7%; Score 123.5; DB 4; Length 573;
Best Local Similarity 17.5%; Pred. No. 0.022;
Matches 85; Conservative 84; Mismatches 209; Indels 109; Gaps 15;

QY 15 DPEODLGEV--FTIYSENERMSAEGLLKFLHTEOGVDFTLDD----- 56
Db 32 DGKVDLLATVTKLELKTSDKNNNGSVLEGVKADKSKVKLTISDDLQOTTFLEVKEDGKT 91
QY 57 --AKQIMERIRKDWKKSF-----GLASINSLSKEAFRKYLMN 92
Db 92 LVSKKVTISKDKSSTEERKEKGEVSEKIITRADGTRELYTGIKSDGSKAKELVKGYVLE 151
QY 93 PDLNGVLHVHQDMTQPMSHYFIFTGHNLYLTGNLSSDSDTPIAAALRRGVRVVELD 152
Db 152 GTLTAERTTLVKBGTVTLSKNISKSG-----EVSVELNDTSSAATKTA----- 197
QY 153 LWPDDKGMKMTGNTLTNPVSQKCVTAIKNNAFTSEY-----PVCVTIEDHL 202
Db 198 AWNSGTSTLITVNSKTKDLV-----TKENTIVQQYDSNGTKLEGSVAEITKLEI 251
QY 203 TSELQGHAAELQIL-----GDALYYPPTTDALVEFPSPESLKRKIIISTKPKR 252
Db 252 KNALKGHPMD--EKLLSKDKKASKDKGKALDLDRELNSKASSKEKSKAKEEITKKSQK 309
QY 253 EYLEACSTQKLAMENRLVEELEKEDKLEQTTTAPLEE-----NHILGENTPSLR 302
Db 310 SLGDLNNDENLMPEDQKLPKLVKLDKKE--FKPVSEVEKLDKIFKSNNNVGLSPLDK 367
QY 303 KEVELSQKEMSTPAELN--SRSPSGLGEATSTRYSKSDGNDGNPKHF-----KYARLI 354
Db 368 SSYKIDSKEETVKNQVNLQKTRPOVKDQVTSNEDLTMSIDSSSPVLEVIDPTNGLG 427
QY 355 TIRLAKHAKGTSMEHRLQVDVESVKRISLSLESKEKLVVEKWEALVFTOKNIRLVYPAAN 414
Db 428 TLQLIDLNTGVLKKESTQ--QGIQRYGIYERKDLVVKMDSGKAKL---QILDKLENLK 482
QY 415 RVNSNF 421
Db 483 VVSESNF 489

RESULT 4

US-08-328-254-6
; Sequence 6, Application US/08328254
; Patent No. 5710022
; GENERAL INFORMATION:
; APPLICANT: Zhu, Xueliang
; APPLICANT: Lee, Wen-Hwa
; TITLE OF INVENTION: A No. 5710022el Nuclear Mitotic Phosphoprotein
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/328,254
;; FILING DATE: 24-OCT-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/141,239
;; FILING DATE: 22-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Campbell, Cathryn A.
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-CJ 1191
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2482 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-328-254-6

Query Match 3.6%; Score 120; DB 1; Length 2482;
Best Local Similarity 21.4%; Pred. No. 0.46;
Matches 129; Conservative 79; Mismatches 216; Indels 178; Gaps 31;

QY 37 EGLLKFLHTGQGDVFTLDDAKQIMERIRKDWKKSFGLASINSLSKEAFKRYLMNPDLN 96
DB 104 EHKQLLSNEIMDKRCYQDLHAEYSLR-----DLLKSKDASLVNED-- 147
QY 97 GVLHNVVHQ-----DWTQPMHSYFIFTGHNSYLTGNLSLSSDSTPIAAALRRGVRVVE 150
DB 148 -----HQSLLAFDQQPAMHHSF-----ANIIEGQSMPS-----ERSECRLE 185
QY 151 LDLPDDKGGMKVTHGNTLTNPVSFKCVTAIKNNAFTSEYPCVVTIEDHLTSELQCHA 210
DB 186 ADQSPKN-----SAILQNRVDSLEF--SLESQKQMSDLQKQC 221
QY 211 AEILEQILGDALYPPPTDALVE--FPSPELKRKIIIST--KPPKEYLEACSTOKLAME 266
DB 222 EELV-QIKGE-----IEENLMKAEQMHQSFAETSQRISKLEQEDTSAHQNVVAE 269
QY 267 NRNLVEELEKE-----DKLEQTTFAPLEE-----NHILGENTPRLKEVEVLS--QKEMST 315
DB 270 TSLALENKEKELQLLNDKVE--TEQAEIQELKSNHLLSDLSKELQLSETLSLEKKEKMS 328
QY 316 PAELNSRSPDLGEATSTRYSKNDGNPKHFKYARLITIRLAKHAKGTSMEHRLQVDE 375
DB 329 IISLNKREIBELTQENG--LKEINASLNQEKMNLIQ-----KSESFAN--YIDE 374
QY 376 SVKRIS-LSFS-KLEKVV-----EKWPEALVKFTOKNIRLVYPAANRVNS-----NFCP 423
DB 375 REKISLSQYKQEKLLILQRCETGNAYEDLSQK-----YKAAQEKSKLECLINECT 429
QY 424 TLAWNTYGAOMVAQMOGYKELMQAFK-----FKNGGCGGVILKPYLLLENLPS 473
DB 430 SL-----CENRKNELQLEAKFAKEHQEPLTKLFAEBERNQMLLETVQQAIRS 480
QY 474 GVPFNTPSPRNTLILKIKVMTLGDWDAFSAKRFHDFSPDPDFTRVIVGVPADEAKWK 533
DB 481 EMTDNQNSKSEAGGLKQELTMTLKEEQNKMQKEVNDLQLENEQLMKVM-----K 529
QY 534 TSVVDSNWAHPHNEDEHAFKCPAL--LRIEVRDHD--SKDEFEQGTCLPIHEVR-D 589
DB 530 TK-----HE-----CNLESEPIRNSVKRESERNQCNKQMDLEVKREISLD 572
QY 590 GY 591
DB 573 SY 574

RESULT 5
US-08-353-700-1

;; Sequence 1, Application US/08353700
;; Patent No. 5599919
;; GENERAL INFORMATION:
;; APPLICANT: YEN, TIMOTHY J.
;; APPLICANT: RATTNER, JEROME B.
;; TITLE OF INVENTION: NUCLEIC ACID ENCODING A
;; TITLE OF INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,
;; TITLE OF INVENTION: AND METHODS OF USE
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: DANN, DORFMAN, HERRELL AND SKILLMAN
;; STREET: 1601 MARKET STREET, SUITE 720
;; CITY: PHILADELPHIA
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103-2307
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/353,700
;; FILING DATE: 09-DEC-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: REED, JANET E.
;; REGISTRATION NUMBER: 36,252
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 563-4100
;; TELEFAX: (215) 563-4044
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3248 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: HUMAN
US-08-353-700-1

Query Match 3.6%; Score 120; DB 1; Length 3248;
Best Local Similarity 21.4%; Pred. No. 0.71;
Matches 129; Conservative 79; Mismatches 216; Indels 178; Gaps 31;

QY 37 EGLLKFLHTGQGDVFTLDDAKQIMERIRKDWKKSFGLASINSLSKEAFKRYLMNPDLN 96
DB 736 EHKQLLSNEIMDKRCYQDLHAEYSLR-----DLLKSKDASLVNED-- 779
QY 97 GVLHNVVHQ-----DWTQPMHSYFIFTGHNSYLTGNLSLSSDSTPIAAALRRGVRVVE 150
DB 780 -----HQSLLAFDQQPAMHHSF-----ANIIEGQSMPS-----ERSECRLE 817
QY 151 LDLPDDKGGMKVTHGNTLTNPVSFKCVTAIKNNAFTSEYPCVVTIEDHLTSELQCHA 210
DB 818 ADQSPKN-----SAILQNRVDSLEF--SLESQKQMSDLQKQC 853
QY 211 AEILEQILGDALYPPPTDALVE--FPSPELKRKIIIST--KPPKEYLEACSTOKLAME 266
DB 854 EELV-QIKGE-----IEENLMKAEQMHQSFAETSQRISKLEQEDTSAHQNVVAE 901
QY 267 NRNLVEELEKE-----DKLEQTTFAPLEE-----NHILGENTPRLKEVEVLS--QKEMST 315
DB 902 TSLALENKEKELQLLNDKVE--TEQAEIQELKSNHLLSDLSKELQLSETLSLEKKEKMS 960
QY 316 PAELNSRSPDLGEATSTRYSKNDGNPKHFKYARLITIRLAKHAKGTSMEHRLQVDE 375
DB 961 IISLNKREIBELTQENG--LKEINASLNQEKMNLIQ-----KSESFAN--YIDE 1006

us-09-828-447-12.rai

Db 292 SWLETNQGLKTKDDLOWALVKDKISLSYD-WYSPNSKVNTSOILTKSKFKDLDLS 350
 QY 135 DTPAAALRRGVVVDLWPD-DKGGMKVTHGNTLNPVSFOKCVTA-IKNA-----F 187
 Db 351 ENF--FLNTKIGTVYLSIIPKLLDPSQISVDKKLVENOKIRFEITASLRAIDKKE 408
 QY 188 FTSEYPCVCTI-----EHLTSELOGHAAEILEQILGD 220
 Db 409 IIOQLPVVDLKVDFNKYQAAVQMGFTIKAVKEFSMPEDQAKTLSN--EIKQV--D 464
 QY 221 ALYVPPTDALVEFSPSLKRIIISTKPKREYLEACSTOKLWENRNLVELEKEDKL 280
 Db 465 RLFEAKTVTNLENFSEVLKSYLLNT---GKYLVDQDQKVKQELKTVIEGLSKANT 521
 QY 281 EOT-----TFAPLENHILGENTPSPRLKREVEVLKEMSTFAELNRSRSDL 327
 Db 522 OKTEKNSPTOKKPEVSLAKTTSNTAKTVKYSTFAEAKGOSQOQTOPVSTSPQSON 581
 QY 328 GENTSTRYSKSDNDNPKH-----FKYARLITIRLAKHAKGTSMEHRLQVDESVKRI 380
 Db 582 SLNST--SSNSVLENEKFTSITWAFNEFI-----YLENTKSEYEI 624
 QY 381 SLSEKSL---EKVKEPEALVKFTQKILNIRVYPAANKVNSNFCPTLAWNYGAQWVAQ- 436
 Db 625 STLGNKLFDFKLVKDNQNLIAOSKISLN---NIINSNKSAYDIKIFNPDPVLDG 679
 QY 437 --NMQYKKEIWAQFKFGKNGGCGYVLPQYILLEML 471
 Db 680 TINTONQGD-----KAEFILKDL 698

RESULT 8

US-07-977-434-8
 ; Sequence 8, Application US/07977434
 ; Patent No. 5466591
 ; GENERAL INFORMATION:
 ; APPLICANT: Gelfand, David H.
 ; APPLICANT: Abramson, Richard D.
 ; TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
 ; NUMBER OF SEQUENCES: THERMOSTABLE DNA POLYMERASES
 ; CORRESPONDENCE ADDRESS: 38
 ; ADDRESSEE: Hoffmann-La Roche Inc.
 ; STREET: 340 Kingsland Street
 ; CITY: Nutley
 ; STATE: New Jersey
 ; ZIP: 07110-1199

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: 7
 SOFTWARE: Wordperfect 2.1
 CURRENT APPLICATION DATA:
 FILING DATE: US/07/977,434

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 FILING DATE: US 590,490
 APPLICATION NUMBER: 28-SEP-1990

FILING DATE: 28-SEP-1990
 APPLICATION NUMBER: US 590,466
 FILING DATE: 28-SEP-1990

APPLICATION NUMBER: US 590,213
 FILING DATE: 28-SEP-1990

APPLICATION NUMBER: US 523,394
 FILING DATE: 15-MAY-1990

APPLICATION NUMBER: US 143,441
 FILING DATE: 12-JAN-1988

APPLICATION NUMBER: US 063,509

Query Match

Best Local Similarity 3.4%; Score 113.5; DB 1; Length 834;
 Matches 114; Conservative 87; Mismatches 195; Indels 221; Gaps 29;

QY 14 GDPEODL-----VGEVFTIYSENERMSAEGLLKFLHTEQGVDFDILDDAK--QIMERIR- 65
 Db 188 GDPSDNLPGVGIGERTALKLLKENGSLNLR-----NLDVVKPESVREIRA 236
 QY 66 --KDWKKSFGASINSL-----SKEAFKYLMPDNLGVHNVHVDMDTOPM 111
 Db 237 HLEDLKLSELSRVSRSDLPLEVDFAFRREPREDGLRAFLERLEFGLHLLHEFGLLEAPAPL 296
 QY 112 SHYFTTGHNSYLTGNLSSDSDTPIAALRRGVVVELDLPDDKGMKVTGNTLTN 171
 Db 297 -----EAP-----WPPPEGAFV---GFVLSR 315
 QY 172 PVSF---OKCVTAIKNAFFTSEYPCVCTIEDHLTSELOGHAAEILEQI-IGDALYYPPT 227
 Db 316 PEPMAELKALAAKEGVRHRAKDPL-AGLD--LKEVRLAKDLAVLALREGDLAPS 372
 QY 228 TDALV-----EFPSPESLKRKIIISTKPKREYLEACSTOKLAME--NRNLVEELEKED 278
 Db 373 DDPMLLAYLLDPSNTTPEGVARRY-----GWEDEDAHRAALLAERLOQNLRLKKEE 426
 QY 279 KL-----EOTTFAPLEENH-----LGENTPSPRLKREVEVLKEMST 315
 Db 427 KLLWLYQEVKPLSRVLAHMEATGVRDVAYLKALSLELAISEIRLEEYFRLA----CH 482
 QY 316 PAELNRSRPSD-----LGEATSTRYSKSDNDGNPKFKYARLITIRLAKHAKG 364
 Db 483 PFNLNSROQLERVLDELRLPALGKTQKT--CKSTSNVLEALREAHPIVEKILQHREL 540
 QY 365 TSWEH-----RL-----QVDESVKRISLESKLEKVEK----- 393
 Db 541 TKLKNYVVDPLPGLVHPRTGRUHTFRNOTATGRUSSDPNLPNIPIRTPLQORIRRAF 600

US-07-977-434-8
 MOLECULE TYPE: protein

QY 394 -----WPEALVKFTQ-----KNILRVYPAANRVNNSNPCPTLANNYGA--QMV 434
Db 601 VAEAGWALVALDYSQIELRVLAHLSGDNILRVFQEGKDIHQ-----TASWFMFGVSPEAV 656
QY 435 AQNMQGYGKELWQAFKFGKNGCGGVYKPKQVYLLNLPSPGVFNFTSPRNTTLILKIKVM 494
Db 657 DPLMRAAKTV-----NFGVLYGMSAHLRSOEL--AIPEEA----- 691
QY 495 TTLGWDKAFSKRHFDLF 511
Db 692 -----VAFIERVQSF 702

RESULT 9
US-08-458-819-8
; Sequence 8, Application US/08458819
; Patent No. 5795762
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; APPLICANT: Abramson, Richard D.
; TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
; TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: 7
; SOFTWARE: Wordperfect 2.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,819
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/977,434
; FILING DATE: 23-FEB-1993
; APPLICATION NUMBER: US 590,490
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,466
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,213
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 523,394
; FILING DATE: 15-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 143,441
; FILING DATE: 12-JAN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 063,509
; FILING DATE: 17-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,241
; FILING DATE: 22-AUG-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 746,121
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US90/07641
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 585,471
; FILING DATE: 20-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 455,611
; FILING DATE: 22-DEC-1989

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 609,157
;; FILING DATE: 02-NOV-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 557,517
;; FILING DATE: 24-JUL-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Luann Cseri
;; REGISTRATION NUMBER: 31,822
;; REFERENCE/DOCKET NUMBER: Case No. 5795762 8753
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (510) 814-2972
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 834 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-458-819-8

Query Match 3.4%; Score 113.5; DB 1; Length 834;
Best Local Similarity 18.5%; Pred. No. 0.3;
Matches 114; Conservative 87; Mismatches 195; Indels 221; Gaps 29;

QY 14 GPEODL-----VGEVFTIYSENERMSAEGLLKFLHTEQGDVDFLDDAK--QIMERIR- 65
Db 188 GPPSDNLPQVGKIGEGTAKLLKKGWLENILK-----NLDVRKVPESVERIKA 236
QY 66 ---KDWKKSFGLASINSDL-----SKEAFKYLMPDNLGVHNVVHODMTOPM 111
Db 237 HLEDLKLSELSRVSRLPLEYDFARRPREDRGRLARLELFSGLSLHLEPAPL 296
QY 112 SHVFTIGHNSYLTGNQLSSDSDTPIAAALRRGVVVELDLPDDKGMKMYTHGNTITN 171
Db 297 -----EAP-----WPPPEGAFV---GFVLSR 315
QY 172 PVSF---QKCVTAIKNAFTSEYPCVTVIEDHLTSELOCHAAEILEQI-LGDALYYPT 227
Db 316 PEPMAELKALAAKCKEGRVHRADPL-AGLKD--LKEVRGLLAKDLAVIALREGDLAPS 372
QY 228 TDALV-----EFPSPESIKRKIIISTPKPEYLEACSTOKLAME--NRNLVEELEKED 278
Db 373 DDPMLLAYLLDPSTNTPGVARRY-----GSEWTEAAHRAALLAERLQONLLERLKGE 426
QY 279 KL-----EQTTFAPLENHI-----LGENTPSLRKEVEVLSOKEMST 315
Db 427 KLLWLYQEVKPLSRVLAHMEATGVRLDVAYLKALSLELAEEIRLEEVEFRLA----GH 482
QY 316 PAELNSRSPSD-----LGEATSTRYKSDNGDNPNKPKFYARLITIRLAKHAGK 364
Db 483 PFNLSRDQLERVLFDLRLPALGKTOKT--GKRSTSAAVLEALRAHPIVEKILQHREL 540
QY 365 TSMEH-----RL-----QVDESVKRISLSSEKLEKVEK----- 393
Db 541 TKLNTYVDPLPGLVHPRTGRLHTRFNQATATGRLLSSDPNLQNPITRPLQRIIRAF 600
QY 394 -----WPEALVKFTQ-----KNILRVYPAANRVNNSNPCPTLANNYGA--QMV 434
Db 601 VAEAGWALVALDYSQIELRVLAHLSGDNILRVFQEGKDIHQ-----TASWFMFGVSPEAV 656
QY 435 AQNMQGYGKELWQAFKFGKNGCGGVYKPKQVYLLNLPSPGVFNFTSPRNTTLILKIKVM 494
Db 657 DPLMRAAKTV-----NFGVLYGMSAHLRSOEL--AIPEEA----- 691
QY 495 TTLGWDKAFSKRHFDLF 511
Db 692 -----VAFIERVQSF 702

RESULT 10
PCT-US91-07035-8
; Sequence 8, Application PC/TUS9107035

OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION: PatentIn Release #1.0, Version #1.30
 APPLICATION DATA:
 FILING DATE: US/09/026,343
 CLASSIFICATION: Herewith
 PRIOR APPLICATION DATA:
 FILING DATE: US 60/038,447
 ATTORNEY/AGENT INFORMATION:
 NAME: GOLDSTEIN, JORGE A.
 REGISTRATION NUMBER: 29,021
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 372-2540
 INFORMATION FOR SEQ ID NO: 2:
 LENGTH: 640 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-026-343-2

Query Match
 Best Local Similarity 3.24; Score 107; DB 3; Length 640;
 Matches 91; Conservative 73; Mismatches 151; Indels 174; Gaps 24;
 QY 9 SCTPKGPOEDLVCEFTI--YSENE---RMSAEG-----LLKFLHTEQGDVD 51
 Db 198 SSTSQRPRDRVHLLALKAYKPELLARLQDGVNQNKSLGAILQOYANLNSKLS 257
 QY 52 FTLDLAKQMERIRKDKW--KSEGLASINDLSKFAFRKYLWNPDLGVHNVVHDMQ 109
 Db 258 YTLKD--VVFELQDMPGYSEIDRSLSVLSRK-----LNPSONA----- 297
 QY 110 PMSHYFITGHSNLTGNLSSD---SDTFIAAALRRGVVVELDLPDDKGGKMTVHG 166
 Db 298 -----TGTSRSPVCSRDVSSPKRLDSEFDPLMNKA--RISH- 339
 QY 167 NLTNPVPSQKCVTAIKNAFFTEYPCVTTIEDHLTSELOHAAEILQILGDALYPP 226
 Db 340 --LTNRV-----PTLNGHLNPTSEKSA-----GLPLFP 367
 QY 227 TTDALVEPSPESLKRKILISHPK-----EYLEACSTQKLM---ENNLVEE 273
 Db 368 AAAL--PTPPLPSTYLPISHPQIVNSNSPSTPGRTQDLPVDSFQNDIYE- 423
 QY 274 LEKEDLEQTF-----APLEENHILG-----ENTPSLRKEVEV 307
 Db 424 -DQDKYTSRTSLETLPGLSVLLKCPKPMENHSHKSKKSKKHKKEDQIKKHDIET 482
 QY 308 LSOKEMSTP-----AELNSRSPDLG-----EATST-----RYSKSN 339
 Db 483 IEKEEDLKREEEIAKLNSSPSSGGVKEDCTASMEPSAIELPDYLYKIYAIYSYEQRQ 542
 QY 340 DQND--NPKHFYARLITIRLAKHAKTSMHR-LOVDESVKRISLESKLEKVEKWEPE 396
 Db 543 NYKDDFNAEYDEYAL-----HARMEVARRFKLDAQRKLSPGSKSKEYQNVHEVLIQ 595
 QY 397 ALVKTQKN 405
 Db 596 EYQIKQSS 604

RESULT 12
 US-07-977-434-10
 ; Sequence 10, Application US/07977434
 ; Patent No. 5466591
 ; GENERAL INFORMATION:
 ; APPLICANT: Gelfand, David H.
 ; APPLICANT: Abramson, Richard D.

TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hoffmann-La Roche Inc.
 STREET: 340 Kingsland Street
 CITY: Nutley
 STATE: New Jersey
 ZIP: 07110-1199
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: 7
 SOFTWARE: WordPerfect 2.1
 CURRENT APPLICATION DATA:
 FILING DATE: US/07/977,434
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 590,490
 FILING DATE: 28-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 590,466
 FILING DATE: 28-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 590,213
 FILING DATE: 28-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 523,394
 FILING DATE: 15-MAY-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 143,441
 FILING DATE: 12-JAN-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 063,509
 FILING DATE: 17-JUN-1987
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 899,241
 FILING DATE: 22-AUG-1986
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 746,121
 FILING DATE: 15-AUG-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US90/07641
 FILING DATE: 21-DEC-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 585,471
 FILING DATE: 20-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 455,611
 FILING DATE: 22-DEC-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 609,157
 FILING DATE: 02-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 557,517
 FILING DATE: 24-JUL-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Luann Cseri
 REGISTRATION NUMBER: 31,822
 REFERENCE/DOCKET NUMBER: Case No. 5466591 8753
 TELEPHONE: (510) 814-2972
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 834 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-977-434-10

Query Match

3.18; Score 104.5; DB 1; Length 834;

DATE: 04-JUN-1993

FILING APPLICATION: 536
 CLASSIFICATION DATA:
 PRIOR APPLICATION NUMBER: US 07/986,330
 APPLICATION DATE: 07-DEC-1992
 FILING DATE: 07-DEC-1992
 FILING OFFICE: 37
 ATTORNEY/AGENT, Peter G.
 NAME: CARTON NUMBER: 32, FORS-00613
 REGISTRATION NUMBER: 837
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/705-8410
 TELEFAX: 415/397-8338 6:
 INFORMATION FOR SEQ ID NO: 6:
 INFORMATION CHARACTERISTICS:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 834 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 09-073-384C-6

MOLECULE TYPE: P-
US-08-073-384C-6
DB 1; Length 834;
30;

[illegible]

RESULT 14
US-08-254-359A-6

	Best Local Similarity	18.59;	pred. NO. 1.9;	Indels	229;	Gaps	30;
	Matches	115,	Mismatches	191;			
OY	14	GDPEODL-----VGEFTTYSIENERSAGLLFLHTEQGDVDFTLDOK--OIMERIR- 65					
		: : :					
Db	188	GPSDNLPGVKIGEGEKATALLKEMGSLNLIK-----NLDRVKPENVRKIRA 236					
		: : :					
OY	66	--KMKKSFGLASINSDL-----SKEAFRYLANPOLNGSVLRNVVVHVHODMTQPM 111					
		: : :					
Db	237	HLEDRLRLSLSRVRTDLPLEVDLAQGREDPREGLRAEFLERLEPGSLGHFGLLEAPAL 296					
		: : :					
OY	112	SHVFIFTCHNSYLTGNOSSDDPTAAALRGCVVVELMDWPDGRGGMKVTHGNLTIN 171					
		: : :					
Db	297	---EEAP-----WPPPEGAFV-----GVILSR 315					
		: : :					
OY	297	-----ETLOQLIG 219					
		: : :					
Db	172	PVSF--QKCVTAKNNRAFTSEYPVCVTIEDHLTSLOQHAA-----ELQGLDVP 372					
		: : :					
OY	316	PEPMAELKALACRGVRHRAADPL-AGLK-LKEVRGBLLARDLAVLASREGLDLVPG 372					
		: : :					
Db	220	DALYYPTTDALVEFFS-----PESIKRKIIITSTPKPYELEACSTQKLABE--NRNLVBEL 274					
		: : :					
OY	220	DALYYPTTDALVEFFS-----PESIKRKIIITSTPKPYELEACSTQKLABE--NRNLVBEL 274					
		: : :					
Db	373	D--DPMLLAYLDPSTTPTEGVARRY-----GGEWEDAARHALLSERLHRNLLKRL 422					
		: : :					
OY	275	EKEDKI-----EOTTFAPLEENHI-----LGENTPSLRKKEVYLSOK 311					
		: : :					
Db	423	BGERGLWLHYHEVEKPLSRVLAHWEATGYRLDVDATLQALSLELAABEIRLEEVEFLA-- 480					
		: : :					
OY	312	EMSTPAELNSRSPD-----LGEATSTRYSKSDGNDGNPHKFYARLTIRLAK 360					
		: : :					
Db	481	--GHFPNLSRDQLERVLFDELRLPALCKTKT--CKRSTSAAVLEALREAHFIVEKILQ 536					
		: : :					
OY	361	HAKGTSMER-----BL--QVDESVKRISLSBESLKKVVEK----- 393					
		: : :					
Db	537	HRETLKNTTYVDPLSLVHPTRGRLHTRFNQTATGRLSSSDPNLONIPVTPPLQRI 596					
		: : :					
OY	394	-----WPEALKVFQQ-----KNILRYPAANRVNNSNFCTPLANNYGA- 431					
		: : :					
Db	597	RAFVAEAGNALVALDYSQIELRVLAHLSGDENLIIVFOCGKDIIHQ-----TASNMFGVP 652					
		: : :					
OY	432	-QWVAQNMOGYGKELWAOFKGKMGCGCYVLPKPVYLENIPLSGVVPNPPTSPPNTLLIK 490					
		: : :					
Db	653	PEAVDPLMRRAAKTV-----NFGVLYGMSAHLRSQEL--AIPIEEA----- 691					
		: : :					
OY	491	IKVMTTLGWDAFKSRRHDFL 511					
		: : :					
Db	692	-----VAFIERYFSQ 702					
		: : :					

RESULT 13
 US-08-073.384C-6 Application US/08073384C
 ; Sequence No. 5541311
 ; PATENT INFORMATION:
 ; GENERAL INFO: Dahlberg, James E.
 ; APPLICANT: Dahlberg, Victor I.
 ; APPLICANT: Lymanichev, Ann D.
 ; APPLICANT: Brov, Mary Ann D.
 ; TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
 ; TITLE OF INVENTION: POLYMERASE
 ; TITLE OF SEQUENCES: 29
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
 ; STREET: 220 Montgomery Street, Suite 2200
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States of America
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS, Version #1.25
 ; SOFTWARE: Patent In Release
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/073.384C

us-09-828-447-12.ra1

Sun Jul 28 10:34:35 2002

Sequence 6, Application US/08254359A
Patent No. 5614402
GENERAL INFORMATION:
APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
TITLE OF INVENTION: 5' NUCLEASES DERIVED FROM THERMOSTABLE
DNA POLYMERASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAVERTOCK, MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,359A
FILING DATE: 06-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 06-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01000
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-254-359A-6

Query Match 3.1%; Score 104.5; DB 1; Length 834;
Best Local Similarity 18.5%; Pred. No. 1.9;
Matches 115; Conservative 86; Mismatches 191; Indels 229; Gaps 30;
QY 14 GDSQDL-----VGEFTYVSENERMSAEGLLFLHTQGDVDFLDDAK--OIMERIR- 65
DB 188 GDSNLPVKGIGETKALKKLGWGSLENLLK-----NLDVRPENVRKIK 236
QY 66 --KWKKSFGIASNSDL-----SKEAFKYLMPDLNGLVHNHVDHMTQPM 111
DB 237 HLEDRLSLSLRVTDPLVDLAQGRPDREGLRAFLERLEFGSLHFEGLLEAPAPL 296
QY 112 SHYFIFTGHSYLTGNLSDDSDTPAAALRGVRVVDLWDDKGMKVTHTGNTLTN 171
DB 297 -----EEAP-----WPPGAFV---GFVLSR 315
QY 172 PVSF---QKCVTAIKNAFFTSYPCVVTIEDHLTSELOQHAA-----EILEQILG 219
DB 316 PEPWAEKALACRGRVHRAADPL-AGLKD--LKEVRGLAKDLAVLASREGDLVPS 372
QY 220 DALYPPPTDVALVEFFS-----PESLKRKIIISTKPKVEYLEACSTQKLAME--NRNVEEL 274
DB 373 D----DPMLLAYLLDPSNTTPEGVARY-----GGWETDAAHALLSRLHRLNLLKRL 422
QY 275 EKDKL-----EQTTFAPLEENHI-----LGNTPSLRKEVELSQK 311

US-08-384-490-31
Sequence 31, Application US/083844490
Patent No. 5618711
GENERAL INFORMATION:
APPLICANT: Gelfand, David H.
APPLICANT: Lawler, Susanne
TITLE OF INVENTION: Recombinant Expression Vectors and
Purification Methods for Thermus Thermophilus DNA
POLYMERASE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,490
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/148,133
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sias, Stacey R.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 8887
TELEPHONE: (510) 814-2863
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-384-490-31

Query Match 3.1%; Score 104.5; DB 1; Length 834;

Search completed: July 26, 2002, 17:22:14
Job time: 4897 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2002, 15:57:57 ; Search time 37.97 Seconds
(without alignments)
1589.257 Million cell updates/sec

Title: US-09-828-447-12
Perfect score: 3228
Sequence: 1 MCSTACRCSTGPKGDPQDL.....MLPHFQCKCTFQDTAPISS 628

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1338	40.2	553	T06771	phosphoinositide-s
2	1293	38.9	549	T11688	phosphoinositide-s
3	1251.5	37.6	600	T06775	phosphoinositide-s
4	1241.5	37.3	600	T06420	phosphoinositide-s
5	1234	37.1	551	T06777	phosphoinositide-s
6	1225.5	36.8	585	T07425	phosphoinositide-s
7	1219.5	36.6	594	T06467	phosphoinositide-s
8	1202.5	36.1	581	T50841	phosphoinositide-s
9	1194	35.9	605	T50842	phospholipase C2 I
10	1192.5	35.8	565	T07424	phosphoinositide-s
11	1175	35.3	596	T07421	phosphoinositide-s
12	1171.5	35.2	581	S71170	phosphoinositide-s
13	1165	35.0	586	T50843	phospholipase C1 I
14	1155	34.7	584	T49206	phosphoinositide-s
15	1030.5	31.0	526	T05681	phosphoinositide-s
16	748	22.5	531	S54098	1-phosphatidylinos
17	692	20.8	764	S14113	1-phosphatidylinos
18	680.5	20.4	513	T45658	1-phosphatidylinos
19	623.5	18.7	751	T29357	1-phosphatidylinos
20	603.5	18.1	745	PC4183	1-phosphatidylinos
21	600	18.0	801	A44165	1-phosphatidylinos
22	594.5	17.9	709	C28821	1-phosphatidylinos
23	594.5	17.9	756	B28821	1-phosphatidylinos
24	577.5	17.4	756	A55943	1-phosphatidylinos
25	566.5	17.0	895	T32374	hypothetical prote
26	561	16.9	997	I54390	phosphoinositide-s
27	559	16.8	1096	I62358	inositol 1,4,5-tri
28	549.5	16.5	1023	B38932	phospholipase C (E
29	541.5	16.3	1211	S68251	phospholipase C, I

30	535	16.1	1181	2	A43346	1-phosphatidylinos
31	520.5	15.6	1095	1	A31225	phospholipase C (E
32	520	15.6	1176	1	A48047	phospholipase C (E
33	519.5	15.6	1898	2	T42440	phospholipase C ho
34	517	15.5	1210	2	A48001	phospholipase C (E
35	512	15.4	1922	2	T21581	hypothetical prote
36	504.5	15.2	1216	2	A28822	1-phosphatidylinos
37	499.5	15.0	1217	2	A45493	phospholipase C-be
38	499	15.0	1216	2	A28821	1-phosphatidylinos
39	498	15.0	1299	2	T24299	hypothetical prote
40	495	14.9	1051	2	S27002	phospholipase C (E
41	495	14.9	1234	2	S52099	phospholipase C-be
42	495	14.9	1234	2	I38994	phospholipase C-be
43	492	14.8	1418	2	T37264	phospholipase C (E
44	490	14.7	875	1	S66672	phosphatidylinosit
45	482	14.5	1173	1	A53430	1-phosphatidylinos

ALIGNMENTS

RESULT 1

T06771

phosphoinositide-specific phospholipase C (EC 3.1.4.-) P12 - soybean
C:Species: Glycine max (soybean)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C:Accession: T06771

R:Shi, J.; Gonzales, R.A.; Bhattacharyya, M.K.

submitted to the EMBL Data Library, November 1995

A:Description: Phosphoinositide-specific phospholipase Cs contain a C-terminal domain

A:Reference number: Z15800

A:Accession: T06771

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-553 <SHI>

A:Cross-references: EMBL:U41473; NID:g1399302; PIDN:AB03257.1; PID:g1399303
A:Experimental source: cultivar Williams 82; etiolated hypocotyls

C:Superfamily: Arabidopsis thaliana 1-phosphatidylinositol-4,5-bisphosphate phosphodi

bisphosphate phosphodiesterase domain Y homology

C:Keywords: phosphoric diester hydrolase

F:81-223/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X h

Query Match 40.2%; Score 1338; DB 2; Length 553;

Best Local Similarity 47.9%; Pred. NO. 1.5e-77;

Matches 282; Conservative 85; Mismatches 176; Indels 46; Gaps 11;

QY 34 MSAGLLKFLHTEQGDVFTLDDAKQIMERIRKDKKKSFGGLASI-----NSDLSKEAF 86

DB 1 MSADQLLRFLHDHQRHETDCSAEDSNRILDSIIQSRKQNDTNAECDDHHTDNNNGLSLDEF 60

QY 87 RYLMNPDLNGVLHNVVHODMTQPMSHVFIFTGHSYLTGNOLSSDSDPTIAAALRGV 146

DB 61 FRFLVLDVNDPDKSQVHDDMAPLSHFYIYTHNSYLTGNOLSSDSDVPIIKALQGV 120

QY 147 RVVELDLWDD-KGGMKVTHGNTLTNPVSQKCVTAIKNNAFPTSEYPCVVTIEDHLTSE 205

DB 121 RVIELDLPNSTKDDIDVVHGRTLTAPVSLIQLSIKSEYAFVKSIDYPVITLEDHLTPF 180

QY 206 LQGHAAIEQLGALYPTTDLVPEPPESLKRKIIISTKPKVEYLEACSTQKLA 265

DB 181 LQAKVAEMTAQVFGDMLXF-POADSLTEPTTPELSKGRILISITKPKVEYLE- 231

QY 266 ENRNLEVELEKEDKQLQTTTFAPLEENHILGENTSLRREVEVLSQKEMSTPAELNSRPS 325

DB 232 -----KQFKDSEREST-----EE-----GSLSPCPIPELEAVDEK-----LANG---S 267

QY 326 DLGEATSTRYSKSDGNDNPKHKFARLITIRLAKHAKTSMEHRLQVDESVKRLSLES 385

DB 268 DLDEGLNARDKKSQDSAP---EYKRLTIIHAGK-PKG-HYKHLNNVGGVKRLSLEQ 322

QY 386 KLEKVVKEPEALVKFTQKNILRVYPAANRVNSSFNCPTLAWNYGAQVMAQMOGYGREL 445

Db 323 ELEKASATYGSIDIVRFTQKNIIRVYVYKGTTRVTSNYPHIGMYGQAVAFNMGGHCKSL 382
QY 446 WQAFKFKGNGGCGVYVLPKQYLLLENLPGVFPNPTSPRNTTLILKIKVMTTLGWDAKFSK 505
Db 383 WYMQGFRANGGCGVYVKKPAFLIEKPHNEVDPKRALPVKKTLKVKYVNGWSSDFS 442
QY 506 RHFDLSPDFRTRVIVGVPADEAKWKTSVVNSNAPHNEDEHEFALKCPALALLRIEV 565
Db 443 THFDSFPDFYTKVCIIVGVPADEAKWKTIVQDNFPVWDEFEFPLTVPALALLRIEV 502
QY 566 RDHDDSKDEFEGTCLPIHEVRDGYRCMOMYDKGNVKGVLMLFHFQ 614
Db 503 REYDKHEKDDFGGTCLPISELRSKGFRAVFLDQKGBQLKSVKLLMRQ 551

RESULT 2

T06775
phosphoinositide-specific phospholipase C (EC 3.1.4.-) - cowpea
C:Species: Vigna unguiculata (cowpea)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jan-2000
C:Accession: T11688
R:Pham Thi, A.T.; El Maarouf, H.; Gareil, M.; d'Arcy-Lameta, A.; Zuily-Fodil, Y.
submitted to the EMBL Data Library, January 1997
A:Description: Molecular cloning and expression of a phosphoinositide-specific phospholipase C from cowpea
A:Reference number: Z17316
A:Accession: T11688
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-549 <PHA>
A:Cross-references: EMBL:U85250; NID:g1786114; PID:g1786115
A:Experimental source: cultivar EPAGE-1; leaves; clone C7b
C:Genetics:
A:Gene: PLC1
C:Superfamily: Arabidopsis thaliana 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase
bisphosphate phosphodiesterase domain Y homology
C:Keywords: phosphoric diester hydrolase
F:106-248/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X

Query Match 38.9%; Score 1293; DB 2; Length 549;
Best Local Similarity 44.9%; Pred. No. 1.1e-74;
Matches 272; Conservative 85; Mismatches 167; Indels 82; Gaps 10;

QY 12 PKGDPQDLVGEVFTIYSEN-ERMSAGLLKFLHTEQGDVDTLDDAKQIMERIRK-DWK 69
Db 21 PKPPDP---VQKAFSEFSGCASSMSAEHLRLAEHQGEVDTCTVSDSEIQQSRKEDGE 77
QY 70 KSFGLASINSLSKAEAFKRYLMPDLNGVLHNVVHODMTQPMHSYFIFTGHNSYLTGNOL 129
Db 78 TGFDL-----HDFHFLQENDLNVPLKSOVHHDMNAPLSHYFTYGHNSYLTGNOL 128
QY 130 SSDSDTPIAALRRGVVVELDLPD-DKGMKVTHGNTLNPVSKVTCVTAIKNNAPF 188
Db 129 SSDSDAPIKALQGVVVELDLPWNSKNKDDIVVHGRTLTTPVSLRLCLASIKREYAFV 188
QY 189 TSEYPCVTVIEDHTELOCHAEILQILGDALYPTTDLVFPSPESLKRKLIIST 248
Db 189 KSOYPLVITLEDHLPDLOAKVAKMATQVFGELLYH-FQTDLSLTFPSPESLKGRIIST 247
QY 249 KPPKEYLEACSTQKLAMENRNVLVEELEKEDKLEQTTTFAPLEENHILGENTPSPSRKEVEVL 308
Db 248 KPPKEFLES----- 256
QY 309 SOKEMSTPAELNSRSPDLGEATSTRYSKSDNGDNDPKHFKYARLITIRLAKHAKGTSM 368
Db 257 SEKESAE-----EYSSLRENADEQRTDNKRAPEYKRLITIHAGK-PKG-BIQ 301
QY 369 HRLQVDESVKRISLSSEKLEKVVKEKPEALVKFTOKNIRLVYPAANRVNSNFCPTLAWN 428
Db 302 DELKAAGNVRRLSLSEQALEKASESYGADVFRFTNNILRVYPKGTRNLSSNYKPHICWT 361
QY 429 YGAQVVAONMOCYKELWQAFCKFKGNGCGVYVLPKQYLLLENLPGSVFPNPTSPRNTTLI 488

Db 362 YGAQVVAONMOCYKELWQAFCKFKGNGCGVYVLPKQYLLLENLPGSVFPNPTSPRNTTLI 421
QY 489 LKIKVMTTLGWDAKFSKRHFDLSPDFRTRVIVGVPADEAKWKTSVVNSNAPHNEDE 548
Db 422 LKVKYVNGWSSDFSDFSYSPDFYVYKVICIVGVPADEIKKKTSTVSNWFPVWNEE 481
QY 549 HEFALCPALALLRIEVDRHDDSKDEFEGTCLPIHEVRDGYRCMOMYDKGNVKGVL 608
Db 482 FDFPLTVPALALLRIEVDRHDDSKDEFEGTCLPIVSELKSGFRSVPLVDEKDKYKSVK 541
QY 609 MLFHFQ 614
Db 542 LLMRFQ 547

RESULT 3

T06775
phosphoinositide-specific phospholipase C (EC 3.1.4.-) P13 (clone SPM537) - soybean
C:Species: Glycine max (soybean)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C:Accession: T06775
R:Shi, J.; Gonzales, R.A.; Bhattacharyya, M.K.
submitted to the EMBL Data Library, November 1995
A:Description: Phosphoinositide-specific phospholipase Cs contain a C-terminal domain
A:Reference number: Z15800
A:Accession: T06775
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-600 <SHI>
A:Cross-references: EMBL:U41474; NID:g1399304; PID:AA03258.1; PID:g1399305
A:Experimental source: cultivar Williams 82; etiolated hypocotyls
C:Superfamily: Arabidopsis thaliana 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y homology
bisphosphate phosphodiesterase domain Y homology
C:Keywords: phosphoric diester hydrolase
F:108-250/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X

Query Match 37.6%; Score 1251.5; DB 2; Length 600;
Best Local Similarity 45.8%; Pred. No. 5.5e-72;
Matches 272; Conservative 89; Mismatches 202; Indels 31; Gaps 12;

QY 24 VFTIYSENERMSAGLLKFLHTEQGDVDTLDDAKQIMERIRKDWKKSFGLASINSLSK 83
Db 31 LFNEYSENELMTPSHLKRFLVDVQKAEEDAQAIDTSFRHFRRGAG-----LNL 83
QY 84 EAFKRYLMPDLNGVL-HNVVHODMTQPMHSYFIFTGHNSYLTGNOLSSSDSTPIAAL 142
Db 84 ETFFKYLESDDNPPLLPSGHVHDMTLPLSHYFTYGHNSYLTGNOLSSDCSDVPIAL 143
QY 143 RGVVVELDLPD-DKGMKVTHGNTLNPVSKVTCVTAIKNNAPFTSEYPCVTVIEDH 201
Db 144 KGVVVELDLPWNSKSDIDVHGRITLTPVELIRCLRSIKDHAFVASEYPPVITLEDH 203
QY 202 LTSELOCHAEILQILGDALYPTTDLVFPSPESLKRKIIISTKPKKEYLEACSTQ 261
Db 204 LTPDLOAKVAKMATQVFGDIL-FTPNSESKVEFPSPESLKRKIIISTKPKKEYLEAKE 262
QY 262 KLAMENRNVLVEELEKEDKLEQTTTFAPLEENHILGENTPSPSRKEVEVLSQEMSTPAELNS 321
Db 263 K-----GDSQHEKEKGDSEHGKAS--GEDEAMGKEVPSL-KGTTEDYKDNVDEDLND 315
QY 322 RSPDLSGEATSTRYSKSDNGDNDPKHFKYARLITIRLAKHAKGTSMHRLQVD-ESVKRI 380
Db 316 EEEFD-----ESDKSHNEAP---EYRHLTAIHAGK-PKGLVE-CLUKVDPKVRRL 362
QY 381 SLSEKLEKVVKEKPEALVKFTOKNIRLVYPAANRVNSNFCPTLAWNQAQVVAONMOC 440
Db 363 SLSEQALEKASESYGADVFRFTNNILRVYPKGTRNLSSNYNPLIGMMHGAQVAFNMOG 422
QY 441 YGELWQAFCKFKGNGCGVYVLPKQYLLLENLPGSVFPNPTSPRNTTLILKIKVMTTLGW 500
Db 423 YGRLWLMHGMFRANGCGVYVKKPNFLLETGTPDEVFNPKAKLPVKTTLKVTYVMGEGWY 482

QY 501 KAFSRHFDLSPDPDFTRVIVGVPADEAKWKTSDVNSWAPHWNEDHEFALKCPAL 560
 Db 483 YDFKTHFDQYSPDFTYTRVGTAGVNDTMRKTRAIEDNWLPTWNEAFEPFLTPVPEAL 542
 QY 561 LRLEVHDDHDDSKDEFGOTCLPIHEVRDGYRCMOMYDKGNVGLKGLVLMFLHFQ 614
 Db 543 LRLEVHDDHDDSKDEFGOTCLPIHEVRDGYRCMOMYDKGNVGLKGLVLMFLHFQ 596

RESULT 4

T06420 phosphoinositide-specific phospholipase C (EC 3.1.4.-), plasma membrane-associated - soy

N/Alternate names: phosphatidylinositol-specific phospholipase C
 C/Species: Glycine max (soybean)
 C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999

C/Accession: T06420
 R/Shi, J.; Gonzales, R.A.; Bhattacharyya, M.K.

submitted to the EMBL Data Library, April 1995
 A/Description: Characterization of a soybean cDNA that encodes a novel plasma membrane

A/Reference number: Z15665

A/Accession: T06420

A/Status: translated from GB/EMBL/DBDJ

A/Molecule type: mRNA

A/Residues: 1-600 <SHI>

A/Cross-references: EMBL:U25027; NID:G945038; PIDN:AAA74441.1; PID:G945039

A/Experimental source: cv. Williams 82; etiolated hypocotyls

C/Superfamily: Arabidopsis thaliana 1-phosphatidylinositol-4,5-bisphosphate phosphodiester

C/Keywords: phosphoric diester hydrolase

F:108-250/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x hom

Query Match 37.3%; Score 1241.5; DB 2; Length 600;
 Best Local Similarity 45.3%; Pred. No. 2.4e-71;
 Matches 269; Conservative 89; Mismatches 205; Indels 31; Gaps 11;

QY 24 VFTIYSENERMSAEGLLFLHTEQGVDFTLDDAKOIMERIRKDWKKSFGSLASINDLSK 83

Db 31 LFEETSENEFWTPSHLKRFLVEVQEKATEDEAQAIDSFHFRRGAG-----LNL 83

QY 84 EAFRYLMNPDLNGVL-HNVYHDMQTPMSHYFTFGHNSYLTGNQSDSDSTPIAAL 142

Db 84 EFTFYKFLSDNPPLPSHGHHDMTLP LSHYFTFGHNSYLTGNQSDSDSTPIAAL 142

QY 143 RGVVVELDLPD-DKGGMKVTHGNLTNPVSFQKCVTAIKNNAFTSEYPCVVTIEDH 201

Db 144 KRGVRIELDLPNASHNDNIDVLRGTLTPVELIRCLRSIKDHAFAVEYPPVITLEDH 203

QY 202 LTSELOQHAAILQILGALYPPPTDVALVEFPSPESLKRKILITSTPKPEYLEACSTQ 261

Db 204 LTPOLQAKVAEMVTETFGD-LLETPNSVESVKEFPSPESLKRKILITSTPKPEYLEAKE 262

QY 262 KAMENRNLYVEELEKEDKLEQTFAPLEENHILGENTPSPSRKEVEVLSQKEMSTPAELNS 321

Db 263 K-----GDSQHEKEGDDSOHG--KALGDEAWGKEVPSL-KGGTIEDYKDYNDVDLND 315

QY 322 RSPSDLGATSTRYSKSDNDGNPNKHFYARLTITRLAKHAKGTSMEHRLQVD-ESVKRI 380

Db 316 EEFDF-----ESDKSHNEAP---EYRLIAIHAGKPKGG--LAECCLKVDPKVRL 362

QY 381 SLSESLEKVEKPEALVKFTQKILRYVYPANRVNSNFCPTLAWNYGAQVMAQMOG 440

Db 363 SLSEQLKELAAINHQOQIVRTFORNLRVYPKGTTRIDSSNYPNLIQWGHGAQVMAQMOG 422

QY 441 YGKELWQAFKFGKNGCGYVLPQYLLLENLPSCVPNPPTSPRNTTLILKIKVMTLQWD 500

Db 423 YGRSLWLMHGMFRANGCGYVKKPFNLEETCPDDEVENPKAKLPVKTTLKVTVYMGEGY 482

QY 501 KAFSRHFDLSPDPDFTRVIVGVPADEAKWKTSDVNSWAPHWNEDHEFALKCPAL 560

Db 483 YDFKTHFDQYSPDFTYTRVGTAGVNDTMRKTRAIEDNWLPTWNEAFEPFLTPVPEAL 542

QY 561 LRLEVHDDHDDSKDEFGOTCLPIHEVRDGYRCMOMYDKGNVGLKGLVLMFLHFQ 614

Db 543 LRLEVHDDHDDSKDEFGOTCLPIHEVRDGYRCMOMYDKGNVGLKGLVLMFLHFQ 596

RESULT 5

T06777

phosphoinositide-specific phospholipase C (EC 3.1.4.-) P25 (clone SPM537) - soybean

C/Species: Glycine max (soybean)

C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999

C/Accession: T06777

R/Shi, J.; Gonzales, R.A.; Bhattacharyya, M.K.

submitted to the EMBL Data Library, November 1995

A/Description: Phosphoinositide-specific phospholipase Cs contain a C-terminal domain

A/Reference number: Z15800

A/Accession: T06777

A/Status: translated from GB/EMBL/DBDJ

A/Molecule type: mRNA

A/Residues: 1-551 <SHI>

A/Cross-references: EMBL:U41475; NID:G1399306; PIDN:AAB03259.1; PID:G1399307

A/Experimental source: cultivar Williams 82; etiolated hypocotyls

C/Superfamily: Arabidopsis thaliana 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain y homology

C/Keywords: phosphoric diester hydrolase

F:70-212/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x h

Query Match 37.1%; Score 1234; DB 2; Length 551;

Best Local Similarity 45.4%; Pred. No. 6.3e-71;

Matches 272; Conservative 88; Mismatches 171; Indels 68; Gaps 16;

QY 34 MSAGLLKFLHTEQGVDFTLDDAKOIMERIRKDWKKSFGSLASINDLSKFAFRKYL-- 91

Db 1 MTAFLHRSFLAEVQREDNATEEAQAI-----DGHKHLSTFH-RSGLNLESFFNYLF 54

QY 92 --NPDNLGVHNVHDMQTPMSHYFTFGHNSYLTGNQSDSDSTPIAALRGVRV 149

Db 55 HNNPPLPSLG--VHDMSPLSHYFTFGHNSYLTGNQSDSDSTPIAALRGVRV 112

QY 150 ELIDLPDD-KGGMKVTHGNLTNPVSFQKCVTAIKNNAFTSEYPCVVTIEDHLSLQ 208

Db 113 ELIDWPNESKNDVNLHGRTLTSPVALIKLSRIKQHAFAVEYPPVITLEDHLPDQA 172

QY 209 HAAEILQILGALYPPPTDVALVEFPSPESLKRKILITSTPKPEYLEACSTOKLAME 268

Db 173 KVAEMITQTFGDL-FAPTSLSLKEFPSPESLKRKILITSTPKPEYLEAKEVQ----- 224

QY 269 NLVEELEKEDKLEQTFAPLEENHILGENTPSPSR-----KEVE---VLSQKEMSTPAE 318

Db 225 -----EKEEESQOB--KPADDEAWGKEVPSLGGTISDYKNIEDDDVLDDEE----- 270

QY 319 LNSRSPDLGATSTRYSKSDNDGNPNKHFYARLTITRLAKHAKGTSMEHRLQVD-BSV 377

Db 271 -----DIDEAKSRQDADE-----YRLIAIHAGKPKGG--LTECLKVDPDKV 312

QY 378 KRISLESLEKVEKPEALVKFTQKILRYVYPANRVNSNFCPTLAWNYGAQVMAQ 437

Db 313 RLSELSELEKAEATGKEIVRTFORNLRVYPKGTTRITSTNYNPLIGWGHGAQVMAFN 372

QY 438 MQGYGKELWQAFKFGKNGCGYVLPQYLLLENLPSCVPNPPTS---PRNTTLILKIKVMT 495

Db 373 MQGYGRSLWLMQGMFRANGCGYVKKPDLKLLKVPNNVEFDPSPRLPVKTT--LKVTIYM 430

QY 496 TLGWDKAFSRHFDLSPDPDFTRVIVGVPADEAKWKTSDVNSWAPHWNEDHEFALK 555

Db 431 GEGWFLDFKTHFDQYSPDFTYTRVGTAGVNDTMRKTRAIEDNWLPTWNEAFEPFL 490

QY 556 PELALLRIEVRHDDHDDSKDEFGOTCLPIHEVRDGYRCMOMYDKGNVGLKGLVLMFLHFQ 614

Db 491 PELALLRVHEVDNSKDEFGOTCLPIHEVRDGYRCMOMYDKGNVGLKGLVLMFLHFQ 549

RESULT 6
 T07425

us-09-828-447-12.rpr

Sun Jul 28 10:34:36 2002

phosphoinositide-specific phospholipase C (EC 3.1.4.-) - garden pea

N:Alternate names: phospholipase C
C:Species: Pisum sativum (garden pea)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C:Accession: T06467

R:Reddy, M.K.
submitted to the EMBL Data Library, October 1997

A:Reference number: Z15699

A:Accession: T06467

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-594 <RED>

A:Cross-references: EMBL:Y15253; PIDN:CAA75546.1

C:Genetics:

A:Note: plc

C:Superfamily: Arabidopsis thaliana 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y homolog

C:Superfamily: phosphodiesterase domain Y homolog

C:Keywords: phosphoric diester hydrolase

F:112-254/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X

Query Match 36.6%; Score 1219.5; DB 2; Length 594;

Best Local Similarity 44.9%; Pred. No. 5.9e-70;

Matches 272; Conservative 100; Mismatches 187; Indels 47; Gaps 17;

QY 16 PEQDLVGEVFTIYS-ENRMSAEGLLKFLHTEQGDVDFTLDDAKQIMERIRKDWKKSFGSL 74

DB 27 PSQ--IRELYHNSDESAMTASHLQRELIIEVQGDENITENEAGSII-----DGHKHLIS 79

QY 75 ASINSDLSAEAFKRYLMNPDLNGLV-HNVVHODMTQPMHSYFTFGHNSYLTGNQSSDS 133

DB 80 FH-RRGLNLESLKFLFSDNKAFLASRGVHVMSLPSLHYIHTGHSNLTGNQVSSDC 138

QY 134 SDTPIAAALRRGVVVELDLWPD-DKGMKVTGNTNPNVSFOKCVTAIKNAFTSEY 192

DB 139 SDAPIIIVALLRGVRVIELDIPNGSKDDIEVLHGRITLTPVALIKLSIKKEAFVASEY 198

QY 193 PVCVTIEDHTLSLOQHAAILLEQILGDALYPTTDLVFPSPESLKRKIIISTKPPK 252

DB 199 PVVITLEDHTLPDLOAKVAQVMVTFQDILFC-PSSESLEKFPSPDLKRRIISTKPPK 257

QY 253 EYLEACSTOKLAMENRNLEVELEKEDKLEQTTTFAPLEENHILGENTPSLR-KEVEVLSQK 311

DB 258 EYLEA-----KEVQEKELKSGSGDEE--AMGKEVPSLRGGTISDYKNN 301

QY 312 EMSTPAELNSRSPDLGEATSTRYSKNDGNDPNKHFYARLITRLAKHAKGTSMEHRL 371

DB 302 DDDDEDLNEEDSE--EAKSRONGSGE-----YRLIAIHAGK-PKGLVE-GL 348

QY 372 QVD-ESVKRISLSKLEKVEKWEALVKFTOKNLRVYPAANRVNNSNFCPTLAWNYG 430

DB 349 KYDPKVRRLSLSQLEKAAETGYKEIVRTQNRILRVYPOGTRITSSNYNPLGWHMG 408

QY 431 AQMVAAQNMGGYKGLQWAFKFGKNGCGGVYLPQYLLNLPSCVFPNPTS--PRNTTLLI 488

DB 409 AQMVAFNMGGYGRSLWLMHGMFGKNGCGGVYKPKDFLLKGTGPNNEVPDPKASLPKTT-- 466

QY 489 LKIKVMTTLGWDAKFSKRFHDLFSPDFETTRIVVGVPADEAKWTSVDNSNAPHWNE 548

DB 467 LKVTVMGEGYDFDHTHFDQSPDFEYARVGIAGVPDFTIMKKTITVEDSWLPKSNV 526

QY 549 HEFALCPPELALRIEVRDHDSDSKDEFGQTCLPIHEVRDGYRCMOMYDKKGNVLKGV 608

DB 527 FEPLVPELALLRVVEHYDMSKDDFGGQTCPLPWEILRTGIRAVPLHRSKRGKYNV 586

QY 609 MLFHFQ 614

DB 587 LLRFE 592

RESULT 8

T50841

phosphoinositide-specific phospholipase C (EC 3.1.4.-) [imported] - rape

phosphoinositide-specific phospholipase C (EC 3.1.4.-) plc3 - potato

C:Species: Solanum tuberosum (potato)

C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000

C:Accession: T07425

R:Kopka, J.; Pical, C.; Gray, J.E.; Mueller-Roeber, B.

Plant Physiol. 116, 239-250, 1998

A:Title: Molecular and enzymatic characterization of three phosphoinositide-specific pho

A:Reference number: Z16026; MUID:98111496

A:Accession: T07425

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-585 <XOR>

A:Cross-references: EMBL:X94289; NID:g2853038; PIDN:CAA63954.1; PID:g2853039

A:Experimental source: cv. Desiree

C:Genetics:

C:Superfamily: Arabidopsis thaliana 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y homolog

C:Superfamily: phosphodiesterase domain Y homolog

C:Keywords: phosphoric diester hydrolase

F:111-252/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom

Query Match 36.8%; Score 1225.5; DB 2; Length 585;

Best Local Similarity 44.2%; Pred. No. 2.4e-70;

Matches 268; Conservative 90; Mismatches 187; Indels 61; Gaps 14;

QY 21 VGEVFTIYSERNMSAEGLLKFLHTEQGDVDFTLDDAKQIMERIRKDWKKSFGSLASIN-- 78

DB 27 VKNLENSYDNGVMSAENLHRLFLIEVQKEENATLEDAAHLMNH-----DLKILNIF 79

QY 79 --SDLSKEAFKYL---NMPDLNGLVHNVHODMTQPMHSYFTFGHNSYLTGNQSSDS 133

DB 80 HRRGLDLDAFFKYLFIADINPLNKLKLG--IHODNAPLSHFYFTGHSNLTGNQSSDC 137

QY 134 SDTPIAAALRRGVVVELDLWPD-DKGMKVTGNTNPNVSFOKCVTAIKNAFTSEY 192

DB 138 SDVPIIQAALHRGVVVELDIPNSAKDDVEVLHGGITLTPVALIKLSIKKEAFTVSEY 197

QY 193 PVCVTIEDHTLSLOQHAAILLEQILGDALYPTTDLVFPSPESLKRKIIISTKPPK 252

DB 198 PVVITLEDHTLPDLOAKVAQVMVTFQDILFC--SSDSCLEKFPSPDLKRRIISTKPPK 255

QY 253 EYLEACSTOKLAMENRNLEVELEKEDKLEQTTTFAPLEENHILGENTPSLRKEVEVLSQKE 312

DB 256 EYLQA-----KEVNETGAMKGTD-----QTDTEANGREV 284

QY 313 MSTPAELNSRSPDLGEA-TSTRYSKNDGNDPNKHFYARLITRLAKHAKGTSMEHRL 371

DB 285 SDIKARYNDKDDSEGEADSDDEEDPTSQONTAP---EYRLIAIHAGKGGGLS--DWL 339

QY 372 QVD-ESVKRISLSKLEKVEKWEALVKFTOKNLRVYPAANRVNNSNFCPTLAWNYG 430

DB 340 RYDPKVRRLSLSQLEKAAETGYKEIVRTQNRILRVYPOGTRITSSNYNPNFNAWTHG 399

QY 431 AQMVAAQNMGGYKGLQWAFKFGKNGCGGVYLPQYLLNLPSCVFPNPTS--PRNTTLLI 488

DB 400 AQMVAFNMGGYGRSLWLMHGMFGKNGCGGVYKPKDFLLKGTGPNNEVPDPKASLPKTT-- 457

QY 489 LKIKVMTTLGWDAKFSKRFHDLFSPDFETTRIVVGVPADEAKWTSVDNSNAPHWNE 548

DB 458 LKVTVMGEGYDFDHTHFDQSPDFEYARVGIAGVPDFTIMKKTITVEDSWLPKSNV 517

QY 549 HEFALCPPELALRIEVRDHDSDSKDEFGQTCLPIHEVRDGYRCMOMYDKKGNVLKGV 608

DB 518 FEPLVPELALLRVVEHYDMSKDDFGGQTCPLPWEILRTGIRAVPLHNRKGEKYNV 577

QY 609 MLFHFQ 614

DB 578 LLRFE 583

RESULT 7

T06467

R;Kopka, J.; Pical, C.; Gray, J.E.; Mueller-Roeber, B.

C; Accession
B. Konka T

R:Kopka, J.; Pical, C.; Gray, J.E.; Mueller-Roeber, B.
Plant Physiol. 116, 239-250, 1998
A:Title: Molecular and enzymatic characterization of three phosphoinositide-specific phospholipase C (EC 3.1.4.-) PLC1 - potato
N:Alternate names: phospholipase C
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: T07421

Plant Physiol. 116, 239-250, 1998
A:Title: Molecular and enzymatic characterization of three phosphoinositide-specific phospholipase C (EC 3.1.4.-) PLC1 - potato
N:Alternate names: phospholipase C
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: T07421

A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-596 <KOP>
A:Cross-references: EMBL:X93564; NID:g2853040; PIDN:CAA63777.1; PID:g2853041
A:Experimental source: cv. Desiree
C:Genetics:
A:Gene: PLC1
C:Superfamily: Arabidopsis thaliana 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y homolog
A:Keywords: phosphoric diester hydrolase
F:113-253/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X homolog

A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-565 <KOP>
A:Cross-references: EMBL:X94183; NID:g2853036; PIDN:CAA63893.1; PID:g2853037
A:Experimental source: cv. Desiree
C:Genetics:
A:Gene: PLC2
C:Superfamily: Arabidopsis thaliana 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y homolog
A:Keywords: phosphoric diester hydrolase
F:107-248/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X homolog

Query Match 35.3%; Score 1175; DB 2; Length 596;
Best Local Similarity 42.2%; Pred. No. 4.1e-67;
Matches 261; Conservative 100; Mismatches 221; Indels 36; Gaps 12;
6 CC--RSCTPKGDEODLVGEFTIYSENERMSAEGLLKFLHTEQGDVDFTLDDAKQIMER 63
9 CCQRFKFLKEAEPDEIKDLFERSENGIMTAHEHLCKFLKDVQGEENVTKKEAEYVES 68
64 IRDKMKKSGFLASINSDLSKEAFKRYLMNPDNLGV--HNVHODMTOPMSHYFTIGHN 121
69 ALKLVHEHLNIVPHRRKGLNLDGFFRYLFS-DUNVSISTDKKVVHDMTAPLSHYFTISHN 127
122 SYLTGNSLSDSDTPIAAALRRGVVVELDLWPD-DKGGMKVTHGNTLTNPVSFQRCV 180
128 TYLTGNSLSDSDTPIIAALRRGVVVELDLWPD-DKGGMKVTHGNTLTNPVSFQRCV 187
181 AKNNAFTSEYPCVVTIEDHLSLQHAETLQILGDALYYPPTDALVEFPSPESL 240
188 SIKEHAFVASEYPIITLEDHLPDLOAKAAEMVTOVFGDIL-FTCGAECLESPSPESL 246
241 KRKIIITKPKPEYLEACSTQKIAMENRNILVEELEKEDKLEOTTAPLEENHILGENTPS 300
247 KRIIITKPKPEYLE--SKKPEKNGSKGKKSEER-----A 284
301 LRKEVEVLSQEMSTPAELNSRPSDLGEATSTRYSKSDNGNDNPKHFKYARLTIRLAK 360
285 WGAETSDLSQK-MTAYSENKDNQECQDEADSHENPNTQNLAP---EYKHLIAQAGK 340
361 HAKGTSMEHRLQVDE-SVKRISLESSEKLEKVPKPEALVKFTQKNILRVYPAANRVNS 419
341 -SKGPTSEW-LTVDPKIKRISLNEEKLINVALNHGKDLIRFTQRLNLLRIYPKGMVDSS 398
420 NFPCTPLANNYGAQVMAQNGYKELWQAFGKFKGNGCGYVLLKPOVLLLENLPVSGVFPNP 479
399 NYNPLMGWHAQVMAQNGYKELWQAFGKFKGNGCGYVLLKPOVLLLENLPVSGVFPNP 458
480 TSPTNTLLIKTKVMTTLGWDKAFSKRHFDFLSPDPFTTRIVVGVVPADAKWKTSTVDN 539
459 KRLSVKTLTKVYMGKWHLDKFRTHFDAYSPPDFVYVIGIAGVAADSRVKKTKRAIED 518
540 SWAPHNEDHEPALKCPPELALLRIEVRDHDSDSKDEFEGOTCLPIHEVRDGRGCMQMYDK 599
519 NWIPIWNEDEFPLVPELALLRIEVRDHDSDSKDEFEGOTCLPIHEVRDGRGCMQMYDK 578
600 KGNVLKGVLMFLHFOCK 617
579 KGEKYPVKLLMRFEVK 596

RESULT 12
S71170
phosphoinositide-specific phospholipase C (EC 3.1.4.-) - Arabidopsis thaliana
N:Alternate names: phosphodiesterase
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: T07421

Query Match 35.8%; Score 1192.5; DB 2; Length 565;
Best Local Similarity 42.7%; Pred. No. 2.9e-68;
Matches 259; Conservative 98; Mismatches 167; Indels 83; Gaps 14;
21 VGEFTIYSENER-MSAEGLLKFLHTEQGDVDFTLDDAKQIMERIRKDKWKSFGGLASINS 79
27 IKNLFRYSDSGVQNLHRLFLIEIQEKKNASLDNAEAIINHGGSQK-----K 78
80 DLSKEAFKRYL---MNPDLNGLVHNVHODMTOPMSHYFTIGHNSYLTGNSLSDSDT 136
79 GLQIDGFFNCLFSDVNPPLDPKLG--IHHDMPNAPLSHYIYTGHSYLTGNSLSDSDT 136
137 PIAAALRRGVVVELDLWPD-DKGGMKVTHGNTLTNPVSFQRCVTAIKNNAFTSEYPCV 195
137 PIIOALQSRVVELDLWPNKDDKDLIEVLHGRITLTPAVALLKLSIKHEAFSASEYPV 196
196 VTIEDHLSLQHAETLQILGDALYYPPTDALVEFPSPESLKRKIIITKPKPEYL 255
197 ITLEDHLPDLOEKVAMITQTFDMLFSP--SESLKELPSPESLKRKIIITKPKPEYL 254
256 EACSTQKIAMENRNILVEELEKEDKLEOTTAPLEENHILGENTPSLRKEVEVLSQEMST 315
255 QS-----REVKEKDDTKKEAQDDVDE-----EED----- 280
316 PAELNSRPSDLGEATSTRYSKSDNGNDNPKHFK-----YARLTIRLAKHAKGTSMEHR 370
281 -----DEDEDEDEPKSEKAAASEYKRLTIAHAGKGGLS--DW 318
371 LOVD-ESVKRISLESSEKLEKVPKPEALVKFTQKNILRVYPAANRVNSNFCPTLANNY 429
319 LRVDLNVKRRSLSPPELEKAVDTHSKRIIRFTQNLNLLRIYPKGIRVDSNYPDFVGMW 378
430 GAQVMAQNGYKELWQAFGKFKGNGCGYVLLKPOVLLLENLPVSGVFPNPTS--PRNTTL 487
379 GAQVMAQNGYKELWQAFGKFKGNGCGYVLLKPOVLLLENLPVSGVFPNPTS--PRNTTL 437
488 ILKIKVMTTLGWDKAFSKRHFDFLSPDPFTTRIVVGVVPADAKWKTSTVDNWSWAPHNE 547
438 -LKVTYVMDGWDKDFDQFHTIYSPDFYAKLGIAGVADPEVKKRTKMTDNDNIPSWDE 496
548 DHEFALKCPPELALLRIEVRDHDSDSKDEFEGOTCLPIHEVRDGRGCMQMYDKGNVLKGV 607
497 QFEFPLTVPELALLRIKVLVDYNSDKDEFAGOTCLPVAELRQGIKRAVPLYDRKGEKYSV 556
608 LMLHFOQ 614
557 KLLMRFE 563

RESULT 11
T07421
phosphoinositide-specific phospholipase C (EC 3.1.4.-) PLC1 - potato
N:Alternate names: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase
C:Species: Solanum tuberosum (potato)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C:Accession: T07421

us-09-828-447-12.rpr

Sun Jul 28 10:34:36 2002

A:Accession: T50843
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-586 <GOS>
A:Cross-references: EMBL:AF223351; PIDN:AAF33823.1

C:Genetics:
C:Gene: P1C1
C:Superfamily: Arabidopsis thaliana 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x
C:Superfamily: Arabidopsis thaliana 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x
F:111-251/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x

Query Match 35.08; Score 1165; DB 2; Length 586;
Best Local Similarity 42.48; pred. No. 1.7e-66;
Matches 258; Conservative 187; Indels 64; Gaps 17;

21 VGEFTYISERNMSAEGLLKFLHTEQGVDFTLDDAKQIMERKDKWKSFGSLASIN-- 78
Db 27 VKNLFNRYSDNGVYMAENLQRLIEVQKEENASLEDAQGINNLH-----DLKILNIF 79
Qy 21 VGEFTYISERNMSAEGLLKFLHTEQGVDFTLDDAKQIMERKDKWKSFGSLASIN-- 78
Db 27 VKNLFNRYSDNGVYMAENLQRLIEVQKEENASLEDAQGINNLH-----DLKILNIF 79
Qy 79 --SDLSKEAPKYL--MNPDLGVHNVVDHMDTQPMHYFTGHNSYLTGNOLSSDS 133
Db 79 --SDLSKEAPKYL--MNPDLGVHNVVDHMDTQPMHYFTGHNSYLTGNOLSSDS 133
Qy 79 --SDLSKEAPKYL--MNPDLGVHNVVDHMDTQPMHYFTGHNSYLTGNOLSSDS 133
Db 80 HRRGLHDAFFKYLADINPPNP--KRGIHDMNEPLSHVFTYTGHSYLTGNOLSSDS 137
Qy 80 HRRGLHDAFFKYLADINPPNP--KRGIHDMNEPLSHVFTYTGHSYLTGNOLSSDS 137
Db 80 HRRGLHDAFFKYLADINPPNP--KRGIHDMNEPLSHVFTYTGHSYLTGNOLSSDS 137
Qy 134 SDPTIAAALRGVRVVELDIWPD--KGMKVTHGNTLTNPVSFOKVCYATKNNNAFTSEY 192
Db 134 SDPTIAAALRGVRVVELDIWPD--KGMKVTHGNTLTNPVSFOKVCYATKNNNAFTSEY 192
Qy 134 SDPTIAAALRGVRVVELDIWPD--KGMKVTHGNTLTNPVSFOKVCYATKNNNAFTSEY 192
Db 138 SDVPITIALRGVRVIELDIPNSAKDDVEVLHGGTLTPVALIKLRSIKHEAFTVSEY 197
Qy 138 SDVPITIALRGVRVIELDIPNSAKDDVEVLHGGTLTPVALIKLRSIKHEAFTVSEY 197
Db 138 SDVPITIALRGVRVIELDIPNSAKDDVEVLHGGTLTPVALIKLRSIKHEAFTVSEY 197
Qy 193 PVCVTIEDHLSLOCHAAEILEOILGDALYPTTDLALVEFPSPESLKRKIIISTPKK 252
Db 193 PVCVTIEDHLSLOCHAAEILEOILGDALYPTTDLALVEFPSPESLKRKIIISTPKK 252
Qy 193 PVCVTIEDHLSLOCHAAEILEOILGDALYPTTDLALVEFPSPESLKRKIIISTPKK 252
Db 198 PVITLEDHLTPDLQAKVAEI--TQTFGDMFLSPDS--CLKNFPPSPESLKRRLISTKPK 254
Qy 198 PVITLEDHLTPDLQAKVAEI--TQTFGDMFLSPDS--CLKNFPPSPESLKRRLISTKPK 254
Db 198 PVITLEDHLTPDLQAKVAEI--TQTFGDMFLSPDS--CLKNFPPSPESLKRRLISTKPK 254
Qy 253 EYACSTQKLAMENRNLVEELEKEDLEOTTFAPLEENHILGENTPSPESLKRVEVLSKE 312
Db 253 EYACSTQKLAMENRNLVEELEKEDLEOTTFAPLEENHILGENTPSPESLKRVEVLSKE 312
Qy 253 EYACSTQKLAMENRNLVEELEKEDLEOTTFAPLEENHILGENTPSPESLKRVEVLSKE 312
Db 255 EYLAQ-----KEVKEKDSK-----GTESP-----DTEARGREV 283
Qy 255 EYLAQ-----KEVKEKDSK-----GTESP-----DTEARGREV 283
Db 255 EYLAQ-----KEVKEKDSK-----GTESP-----DTEARGREV 283
Qy 313 MTPAELNSRSPDLGEATSTRYSKSDNDNDPKH---KVARLITIRLAKHAKGTSMH 369
Db 313 MTPAELNSRSPDLGEATSTRYSKSDNDNDPKH---KVARLITIRLAKHAKGTSMH 369
Qy 313 MTPAELNSRSPDLGEATSTRYSKSDNDNDPKH---KVARLITIRLAKHAKGTSMH 369
Db 284 SULKARYNDKDDSDGAGVED--DESDGPNSSQONVAPEYKCLIAHAGKGGGSL--D 339
Qy 284 SULKARYNDKDDSDGAGVED--DESDGPNSSQONVAPEYKCLIAHAGKGGGSL--D 339
Db 284 SULKARYNDKDDSDGAGVED--DESDGPNSSQONVAPEYKCLIAHAGKGGGSL--D 339
Qy 370 RLQVD--ESYKRISLSEKLEKVEKWEKPEALVKFTQKNIIRVYPAANRVNSNFCPTLAWN 428
Db 370 RLQVD--ESYKRISLSEKLEKVEKWEKPEALVKFTQKNIIRVYPAANRVNSNFCPTLAWN 428
Qy 370 RLQVD--ESYKRISLSEKLEKVEKWEKPEALVKFTQKNIIRVYPAANRVNSNFCPTLAWN 428
Db 340 WLRVDPKVRRLSLEQELGKAVVTHGKEIIRTORNLRIYKGIKIRPSSNYPFAWT 399
Qy 340 WLRVDPKVRRLSLEQELGKAVVTHGKEIIRTORNLRIYKGIKIRPSSNYPFAWT 399
Db 340 WLRVDPKVRRLSLEQELGKAVVTHGKEIIRTORNLRIYKGIKIRPSSNYPFAWT 399
Qy 429 YGAQVQAQNMVQYKGLKQAFKFGNGCGYVLPKQYLLLENLPSPGVNPTS--PRNT 486
Db 429 YGAQVQAQNMVQYKGLKQAFKFGNGCGYVLPKQYLLLENLPSPGVNPTS--PRNT 486
Qy 429 YGAQVQAQNMVQYKGLKQAFKFGNGCGYVLPKQYLLLENLPSPGVNPTS--PRNT 486
Db 400 HGAQV--HMQGYGRSLWLMHGMFRNGCGYVKKPDILLKAGPNQOIFDPEANLPVKT 458
Qy 400 HGAQV--HMQGYGRSLWLMHGMFRNGCGYVKKPDILLKAGPNQOIFDPEANLPVKT 458
Db 400 HGAQV--HMQGYGRSLWLMHGMFRNGCGYVKKPDILLKAGPNQOIFDPEANLPVKT 458
Qy 487 LILKIKVMTTLGWDKAFSRHFDLSPDPDFTRVIVGVPADEAKWTSYVDNSWAPHN 546
Db 487 LILKIKVMTTLGWDKAFSRHFDLSPDPDFTRVIVGVPADEAKWTSYVDNSWAPHN 546
Qy 487 LILKIKVMTTLGWDKAFSRHFDLSPDPDFTRVIVGVPADEAKWTSYVDNSWAPHN 546
Db 459 --LKVTVFMGGWIDFKHTFDAYTPDPFYAKIGIAGVPADNVMMKTKTLEDMDTPTWD 516
Qy 459 --LKVTVFMGGWIDFKHTFDAYTPDPFYAKIGIAGVPADNVMMKTKTLEDMDTPTWD 516
Db 459 --LKVTVFMGGWIDFKHTFDAYTPDPFYAKIGIAGVPADNVMMKTKTLEDMDTPTWD 516
Qy 547 EDHEFALCPALALLRLEVRDHDSDSKDEFQGTCLPIHEVRDGYRCMOMYDKKGNVKG 606
Db 547 EDHEFALCPALALLRLEVRDHDSDSKDEFQGTCLPIHEVRDGYRCMOMYDKKGNVKG 606
Qy 547 EDHEFALCPALALLRLEVRDHDSDSKDEFQGTCLPIHEVRDGYRCMOMYDKKGNVKG 606
Db 517 EKFEPLTVPELALLRLEVRDHDSDSKDEFQGTCLPIHEVRDGYRCMOMYDKKGNVKG 576
Qy 517 EKFEPLTVPELALLRLEVRDHDSDSKDEFQGTCLPIHEVRDGYRCMOMYDKKGNVKG 576
Db 517 EKFEPLTVPELALLRLEVRDHDSDSKDEFQGTCLPIHEVRDGYRCMOMYDKKGNVKG 576
Qy 607 VLMLFHQ 614
Db 607 VLMLFHQ 614
Qy 577 VKLLMRE 584
Db 577 VKLLMRE 584

RESULT 14
T49206
phospholipase C-like protein - Arabidopsis thaliana
N:Alternate names: protein F27K19, 120
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 28-Jul-2000
C:Accession: T49206
R:Benes, V.; Wurmbach, E.; Drzonek, H.; Ansoorge, W.; Mewes, H.W.; Rudd, S.; Lemcke, K.
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25014
A:Accession: T49206
A:Status: preliminary

C:Accession: S71170
R:Fukunaga, M.; Hanase, A.; Sohnaka, M.; Inoue, H.; Tsuruta, Y.; Nakao, M.
submitted to the EMBL Data Library, June 1995
A:Description: Genetic characterization of borrelia burgdorferi sensu lato from Japanese
C:Keywords: phosphoric diester hydrolase
F:105-248/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain x hom

Query Match 35.28; Score 1171.5; DB 1; Length 581;
Best Local Similarity 43.18; pred. No. 6.5e-67; Indels 83; Gaps 15;
Matches 262; Conservative 178; Mismatches 185

24 VFTIYSERNMSAEGLLKFLHTEQGVDFTLDDAKQIMERKDKWKSFGSLASIN-- 81
Db 30 IFEKYSNGVMTVDHLHRLFDIVQKDKATREDAQSII-----NSASSLHRLHGLH 81
Qy 24 VFTIYSERNMSAEGLLKFLHTEQGVDFTLDDAKQIMERKDKWKSFGSLASIN-- 81
Db 30 IFEKYSNGVMTVDHLHRLFDIVQKDKATREDAQSII-----NSASSLHRLHGLH 81
Qy 84 EAFRYLM--NPDGVHNVVDHMDTQPMHYFTGHNSYLTGNOLSSDS--SDPTIAA 140
Db 84 EAFRYLM--NPDGVHNVVDHMDTQPMHYFTGHNSYLTGNOLSSDS--SDPTIAA 140
Qy 84 EAFRYLM--NPDGVHNVVDHMDTQPMHYFTGHNSYLTGNOLSSDS--SDPTIAA 140
Db 82 DAFKYLFGDNNPPL--ALHK--VHDMADAPISHYFTGHNSYLTGNOLSSDS--SDPTIAA 138
Qy 82 DAFKYLFGDNNPPL--ALHK--VHDMADAPISHYFTGHNSYLTGNOLSSDS--SDPTIAA 138
Db 82 DAFKYLFGDNNPPL--ALHK--VHDMADAPISHYFTGHNSYLTGNOLSSDS--SDPTIAA 138
Qy 141 ALRRGVVVELDLPD--DKGCMKVTHTNTLTNPVSFOKVCYATKNNNAFTSEYVCTIE 199
Db 141 ALRRGVVVELDLPD--DKGCMKVTHTNTLTNPVSFOKVCYATKNNNAFTSEYVCTIE 199
Qy 141 ALRRGVVVELDLPD--DKGCMKVTHTNTLTNPVSFOKVCYATKNNNAFTSEYVCTIE 199
Db 139 ALKKGVRVIELDIPNSAKDDVEVLHGGTLTPVALIKLRSIKHEAFTVSEY 197
Qy 139 ALKKGVRVIELDIPNSAKDDVEVLHGGTLTPVALIKLRSIKHEAFTVSEY 197
Db 139 ALKKGVRVIELDIPNSAKDDVEVLHGGTLTPVALIKLRSIKHEAFTVSEY 197
Qy 200 DHTLSELOCHAAEILEOILGDALYPTTDLALVEFPSPESLKRKIIISTPKK 252
Db 200 DHTLSELOCHAAEILEOILGDALYPTTDLALVEFPSPESLKRKIIISTPKK 252
Qy 200 DHTLSELOCHAAEILEOILGDALYPTTDLALVEFPSPESLKRKIIISTPKK 252
Db 199 DHTLPDLQAKVAEI--TQTFGDMFLSPDS--CLKNFPPSPESLKRRLISTKPK 254
Qy 199 DHTLPDLQAKVAEI--TQTFGDMFLSPDS--CLKNFPPSPESLKRRLISTKPK 254
Db 199 DHTLPDLQAKVAEI--TQTFGDMFLSPDS--CLKNFPPSPESLKRRLISTKPK 254
Qy 260 TOKLAMENRNLVEELEKEDLEOTTFAPLEENHILGENTPSPESLKRVEVLSKE 312
Db 260 TOKLAMENRNLVEELEKEDLEOTTFAPLEENHILGENTPSPESLKRVEVLSKE 312
Qy 260 TOKLAMENRNLVEELEKEDLEOTTFAPLEENHILGENTPSPESLKRVEVLSKE 312
Db 259 -----VEVQKG-----KDLGDEEVGVRVPSFIQNK----- 286
Qy 259 -----VEVQKG-----KDLGDEEVGVRVPSFIQNK----- 286
Db 259 -----VEVQKG-----KDLGDEEVGVRVPSFIQNK----- 286
Qy 320 NSRSPDLGEATSTRYSKSDNDNDPKH---KVARLITIRLAKHAKGTSMH 369
Db 320 NSRSPDLGEATSTRYSKSDNDNDPKH---KVARLITIRLAKHAKGTSMH 369
Qy 320 NSRSPDLGEATSTRYSKSDNDNDPKH---KVARLITIRLAKHAKGTSMH 369
Db 287 -SEAKDDL-----DGNDDDDDDDEKSKINAPQTKH--LIAHAGKPGG-- 330
Qy 287 -SEAKDDL-----DGNDDDDDDDEKSKINAPQTKH--LIAHAGKPGG-- 330
Db 287 -SEAKDDL-----DGNDDDDDDDEKSKINAPQTKH--LIAHAGKPGG-- 330
Qy 366 SMEHRLQVD--ESYKRISLSEKLEKVEKWEKPEALVKFTQKNIIRVYPAANRVNSNFCPT 428
Db 366 SMEHRLQVD--ESYKRISLSEKLEKVEKWEKPEALVKFTQKNIIRVYPAANRVNSNFCPT 428
Qy 366 SMEHRLQVD--ESYKRISLSEKLEKVEKWEKPEALVKFTQKNIIRVYPAANRVNSNFCPT 428
Db 331 -ITECLAVDPKVRRLSLEQELGKAVVTHGKEIIRTORNLRIYKGIKIRPSSNYPFAWT 399
Qy 331 -ITECLAVDPKVRRLSLEQELGKAVVTHGKEIIRTORNLRIYKGIKIRPSSNYPFAWT 399
Db 331 -ITECLAVDPKVRRLSLEQELGKAVVTHGKEIIRTORNLRIYKGIKIRPSSNYPFAWT 399
Qy 425 LANNYGAQVQAQNMVQYKGLKQAFKFGNGCGYVLPKQYLLLENLPSPGVNPTS--PRNT 486
Db 425 LANNYGAQVQAQNMVQYKGLKQAFKFGNGCGYVLPKQYLLLENLPSPGVNPTS--PRNT 486
Qy 425 LANNYGAQVQAQNMVQYKGLKQAFKFGNGCGYVLPKQYLLLENLPSPGVNPTS--PRNT 486
Db 390 VGSWGAQVQAQNMVQYKGLKQAFKFGNGCGYVLPKQYLLLENLPSPGVNPTS--PRNT 486
Qy 390 VGSWGAQVQAQNMVQYKGLKQAFKFGNGCGYVLPKQYLLLENLPSPGVNPTS--PRNT 486
Db 390 VGSWGAQVQAQNMVQYKGLKQAFKFGNGCGYVLPKQYLLLENLPSPGVNPTS--PRNT 486
Qy 483 RNTLILKIKVMTTLGWDKAFSRHFDLSPDPDFTRVIVGVPADEAKWTSYVDNSWAPHN 546
Db 483 RNTLILKIKVMTTLGWDKAFSRHFDLSPDPDFTRVIVGVPADEAKWTSYVDNSWAPHN 546
Qy 483 RNTLILKIKVMTTLGWDKAFSRHFDLSPDPDFTRVIVGVPADEAKWTSYVDNSWAPHN 546
Db 450 VKTT--LRVTVFMGGWIDFKHTFDAYTPDPFYAKIGIAGVPADNVMMKTKTLEDMDTPTWD 516
Qy 450 VKTT--LRVTVFMGGWIDFKHTFDAYTPDPFYAKIGIAGVPADNVMMKTKTLEDMDTPTWD 516
Db 450 VKTT--LRVTVFMGGWIDFKHTFDAYTPDPFYAKIGIAGVPADNVMMKTKTLEDMDTPTWD 516
Qy 543 PHNEDHEFALCPALALLRLEVRDHDSDSKDEFQGTCLPIHEVRDGYRCMOMYDKKGN 602
Db 543 PHNEDHEFALCPALALLRLEVRDHDSDSKDEFQGTCLPIHEVRDGYRCMOMYDKKGN 602
Qy 543 PHNEDHEFALCPALALLRLEVRDHDSDSKDEFQGTCLPIHEVRDGYRCMOMYDKKGN 602
Db 508 PAWDEFEPLTVPELALLRLEVRDHDSDSKDEFQGTCLPIHEVRDGYRCMOMYDKKGN 576
Qy 508 PAWDEFEPLTVPELALLRLEVRDHDSDSKDEFQGTCLPIHEVRDGYRCMOMYDKKGN 576
Db 508 PAWDEFEPLTVPELALLRLEVRDHDSDSKDEFQGTCLPIHEVRDGYRCMOMYDKKGN 576
Qy 603 VLKGLML 610
Db 603 VLKGLML 610
Qy 568 KYKSVKLL 575
Db 568 KYKSVKLL 575

RESULT 13
T50843
phospholipase C [imported] - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 18-Aug-2000
C:Accession: T50843
R:Goswami, M.; Singh, B.N.; Reddy, M.K.; Sopory, S.K.
submitted to the EMBL Data Library, January 2000
A:Reference number: Z25259

A:Molecule type: DNA

A:Residues: 1-584 <BEN>

A:Cross-references: EMBL:AL163832; GSPDB:GM00061; ATSP:F27K19.120

A:Experimental source: cultivar Columbia; BAC clone F27K19

C:Genetics:

A:Gene: ATSP:F27K19.120

A:Map position: 3

A:Introns: 100/3; 166/2; 211/3; 290/3; 371/2; 410/3; 458/3; 487/3

C:Superfamily: Arabidopsis thaliana 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom

Bisphosphate phosphodiesterase domain Y homology

F:105-248/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom

Query Match

Best Local Similarity 34.7%; Score 1155; DB 2; Length 584;

Matches 234; Conservative 99; Mismatches 190; Indels 58; Caps 14;

QY 24 VFTIYSENERMSAEGLLKFLTEGGDYDFDLDLIDVQKODKATKEAQDIV-----NASSLLHRRNG-LHL 81

Db 30 LFDNYSDKGLMTDLDLLRLFLIDVQKODKATKEAQDIV-----NASSLLHRRNG-LHL 81

QY 84 EAFKRYLM---NPDLGVHNVVHODTQPMDSHYFTTGHNSYLTGNLSGDSSTPIAA 140

Db 82 DAFKRYLAVTNSPLSL---EVHODMADPLSHYFTTGHNSYLTGNLSGDSSTPIAA 140

QY 141 ALRGVVRVLDLWPD-DKGMKVTHTGNLTNPVSFQKCVTAIKNAFFTSVPVCTIE 138

Db 139 ALRGVVRVLDLWPD-DKGMKVTHTGNLTNPVSFQKCVTAIKNAFFTSVPVCTIE 138

QY 200 DHTLSEQGHAAEILFQILGALYPTTDALVEFPSPESLKRKIIISTKPKKEYLEACS 259

Db 199 DHTLSEQGHAAEILFQILGALYPTTDALVEFPSPESLKRKIIISTKPKKEYLEACS 259

QY 260 TOKLAMENRNLVEELEKEDLEQTTAPLEENHILGENTPSPSRKEVEVLSOKEMSTPAEL 319

Db 258 DDLVKKGRD-----LGDKEVNGREVPSFIRDRSDVNDKNSGDDDD 299

QY 320 NSRPSDLGEATSTRYSKSDNDGNPKHP---KYARLITIRLAKHAGTSMHRLVD-E 375

Db 300 DDDDDDD-----DDGDKIKKNAPPEYKHLIAEAGPKGG--ITECLKVDPD 346

QY 376 SVKRISLSEKLEKVEKPEALVKFTOKNLRVYPAANRVSNFPCPTLANNYGAQVMA 435

Db 347 KVRRLSLESEKLEKVEKPEALVKFTOKNLRVYPAANRVSNFPCPTLANNYGAQVMA 435

QY 436 QNMQGYGKELWQAFKFGKGGCGYVLPQYLLLENLPSGVFPNP--TSRNTTILIKIV 493

Db 407 FNMGLGRSLWQAFKFGKGGCGYVLPQYLLLENLPSGVFPNP--TSRNTTILIKIV 493

QY 494 MTTGLWDAFSAKRHFDLFPDPDEFTRVIVGVPADEAKWTSVVDNSWAPHNEDHEFAL 553

Db 462 YMGEGWYDFPHTHFDYSPDPFTRVIVGVPADEAKWTSVVDNSWAPHNEDHEFAL 553

QY 554 KPELALLRIEVRDHDSDKDEFGOTCLPIHEVRDGYRCOMYDKKGNVLKGVLMFLHF 613

Db 522 TVPELALLRIEVRDHDSDKDEFGOTCLPIHEVRDGYRCOMYDKKGNVLKGVLMFLHF 613

QY 614 Q 614

Db 582 E 582

RESULT 15

T05681

phosphoinositide-specific phospholipase C (EC 3.1.4.-) F20M13.90 - Arabidopsis thaliana

N:Alternate names: protein F20M13.90

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999

R:Accession: T05681

R:Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.R.

Submitted to the Protein Sequence Database, February 1999

A:Reference number: 215420

A:Accession: T05681

A:Molecule type: DNA

A:Residues: 1-526 <BEV>

A:Cross-references: EMBL:AL035540

A:Experimental source: cultivar Columbia; BAC clone F20M13

C:Genetics:

A:Map position: 4

A:Introns: 65/3; 131/2; 176/3; 306/2; 345/3; 422/3

C:Superfamily: Arabidopsis thaliana 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom

Bisphosphate phosphodiesterase domain Y homology

F:70-212/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom

F:256-377/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y hom

Query Match

Best Local Similarity 31.0%; Score 1030.5; DB 2; Length 526;

Matches 234; Conservative 89; Mismatches 179; Indels 93; Caps 15;

QY 34 MSAEGLKFLHTEGGDYDFDLDLIDVQKODKATKEAQDIV-----NASSLLHRRNG-LHL 81

Db 1 MSFDELLRFVSEVGERHAGLDYVQDIFHSVKHNVFHHGLVHLN-----AFYRLF 54

QY 93 PDLNGLV---HNVDHODTQPMDSHYFTTGHNSYLTGNLSGDSSTPIAA 140

Db 55 -DTNSPLPMGQVHHDMKAPLSHYFTTGHNSYLTGNLSGDSSTPIAA 140

QY 151 LDLPDPDKG-GMKVTHGNTLNPVSFQKCVTAIKNAFFTSVPVCTIE 138

Db 114 LDLPDPDKG-GMKVTHGNTLNPVSFQKCVTAIKNAFFTSVPVCTIE 138

QY 210 AAEILFQILGALYPTTDALVEFPSPESLKRKIIISTKPKKEYLEACS 259

Db 174 VAKMLTKTVRGM-LFRVSEFKEFPSPESLKRKIIISTKPKKEYLEACS 259

QY 270 LVEELEKEDLEQTTAPLEE-----NHILGENTPSPSRKEVEVLSOKEMSTPAEL 319

Db 221 -----KTVHTTPTTVKETSNNRVANKILBE-----YKMESEA----- 254

QY 322 RSPSDELGEATSTRYSKSDNDGNPKHP---KYARLITIRLAKHAGTSMHRLVD-E 375

Db 255 -----VGYRDLTAIH-AAACKDPKDCDLSDDPEKPIRV 287

QY 382 LSESKLEKVEKPEALVKFTOKNLRVYPAANRVSNFPCPTLANNYGAQVMA 435

Db 288 MDEQWLDLTVTRGTDLVRFTRQNLRIYKPGTRVDSSNYDPHVGTWGHGAQVMAFNQGH 347

QY 442 GKELWQAFKFGKGGCGYVLPQYLLLENLPSGVFPNP--TSRNTTILIKIV 493

Db 348 GKOLWIMQGMFRGNGCGYVLPQYLLLENLPSGVFPNP--TSRNTTILIKIV 493

QY 500 DKAFSKRHFDFLSPDPDEFTRVIVGVPADEAKWTSVVDNSWAPHNEDHEFAL 553

Db 403 DLDPHHTHFDYSPDPDEFTRVIVGVPADEAKWTSVVDNSWAPHNEDHEFAL 553

QY 559 ALLRIEVRDHDSDKDEFGOTCLPIHEVRDGYRCOMYDKKGNVLKGVLMFLHF 613

Db 463 ALLWFKVQDYDNDQDFAGTCLPLPELKSQVRAVRLHRTGKAYKNTLLVSF 517

Search completed: July 26, 2002, 17:21:37

Job time: 5020 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 26, 2002, 17:21:42 ; Search time 19.78 Seconds
(without alignments)
1229.316 Million cell updates/sec

Title: US-09-828-447-12
Perfect score: 3328
Sequence: 1 MCSIACGSGTGRKPEQDL.....MLFHQKCKCTFQDTAPISS 628

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	600	18.0	801	PIPA_DICDI	Q02158 dictyosteli
2	594.5	17.9	695	PID1_BOVIN	P10895 bos taurus
3	594.5	17.9	756	PID1_RAT	P10688 rattus norv
4	577.5	17.4	756	PID1_HUMAN	P51178 homo sapien
5	549.5	16.5	1023	PIB4_BOVIN	Q07722 bos taurus
6	536.5	16.1	1175	PIB4_HUMAN	Q15147 homo sapien
7	535	16.1	1181	PIB2_HUMAN	Q00722 homo sapien
8	522.5	15.7	1175	PIB4_RAT	Q9q07 rattus norv
9	516.5	15.5	1095	PIPA_DROME	P13217 drosophila
10	506.5	15.2	1234	PIP3_MOUSE	P51432 mus musculus
11	504.5	15.2	1216	PIB1_BOVIN	P10894 bos taurus
12	501	15.1	1216	PIB1_HUMAN	Q9nq66 homo sapien
13	499	15.0	1216	PIB1_RAT	P10687 rattus norv
14	495	14.9	1234	PIP3_HUMAN	Q01970 homo sapien
15	476	14.3	899	PICL_SCHPO	P40977 schizosacch
16	464.5	14.0	1312	PICL_DROME	P25455 drosophila
17	457.5	13.7	1265	PIG2_RAT	P24135 rattus norv
18	448.5	13.5	1252	PIG2_HUMAN	P16885 homo sapien
19	428	12.9	869	PICL_YEAST	P32383 saccharomyc
20	422.5	12.7	1099	PICL_CANAL	O13433 candida alb
21	412.5	12.4	1291	PIG1_BOVIN	P08487 bos taurus
22	409.5	12.3	1290	PIG1_RAT	P10686 rattus norv
23	399	12.0	1290	PIG1_HUMAN	P19174 homo sapien
24	134.5	4.0	1679	YIO9_YEAST	P40457 saccharomyc
25	132	4.0	722	MFPI1_TORAC	Q9m714 nicotiana t
26	128	3.8	1616	PIP2_MYCCE	Q49429 mycoplasma
27	125	3.8	771	SKN1_YEAST	P33336 saccharomyc
28	123.5	3.7	2145	YXAA_PODAN	Q01513 podospora a
29	120	3.6	3210	CENF_HUMAN	P49454 homo sapien
30	119	3.6	3068	POLG_PEMVC	Q01500 p genome po
31	116.5	3.5	556	VIE2_AGR75	P08062 agrobacteri
32	116	3.5	1997	OTOF_HUMAN	Q9hcl0 homo sapien
33	115.5	3.5	1603	VIT5_CAEEL	P06125 caenorhabdi

RESULT	1	34	115	3.5	1545	1	YM2_YEAST	Q03640	saccharomyc
PIPA_DICDI	ID	PIPA_DICDI	STANDARD;	PRT;	801 AA.				
AC	Q02158;								
DT	01-OCT-1993 (Rel. 27, Created)								
DT	01-OCT-1993 (Rel. 27, Last sequence update)								
DT	16-OCT-2001 (Rel. 40, Last annotation update)								
DE	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase								
DE	(EC 3.1.4.11) (PLC) (Phosphoinositide-specific phospholipase C).								
GN	PIPA OR PLC.								
OS	Dictyostelium discoideum (Slime mold).								
OC	Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.								
OX	NCBI_TaxID=44689;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=NC-4;								
RX	MEDLINE=92406741; PubMed=1326523;								
RA	Drayer A.L., van Haastert P.J.;								
RT	"Molecular cloning and expression of a phosphoinositide-specific phospholipase C of Dictyostelium discoideum.";								
RL	J. Biol. Chem. 267:18387-18392(1992).								
CC	-!- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES								
CC	DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS								
CC	MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE								
CC	C ENZYMES.								
CC	-!- CATALYTIC ACTIVITY: 1-phosphatidyl-D-myo-inositol 4,5-								
CC	bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +								
CC	diacylglycerol.								
CC	-!- DEVELOPMENTAL STAGE: EXPRESSED AT ALL STAGES; INCREASE IN								
CC	EXPRESSION IN THE CULMINATING FRUITING BODY AND DURING								
CC	STARVATION.								
CC	-!- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF								
CC	PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.								
CC	-!- SIMILARITY: CONTAINS 1 C2 DOMAIN.								
CC	-!- SIMILARITY: CONTAINS 1 EF-HAND CALCIUM-BINDING DOMAIN.								
CC	-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 IS THE INITIATOR.								
CC	-----								
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/								
CC	or send an email to license@isb-sib.ch).								
CC	-----								
DR	EMBL; M5783; AAA33235.1; -.								
DR	PIR; A44165; A44165.								
DR	HSSP; P10688; 1DJX.								
DR	DictyDb; DD05034; pipa.								
DR	InterPro; IPR000008; C2.								
DR	InterPro; IPR002048; EF-hand.								
DR	InterPro; IPR001192; PI_PLC.								
DR	InterPro; IPR000909; PI_PLC_X.								
DR	InterPro; IPR001711; PI_PLC_Y.								
DR	Pfam; PF00168; C2; 1.								
DR	Pfam; PF00388; PI_PLC-X; 1.								

DR Pfam; PF00387; PI-PLC-Y; 1.
 DR PRINTS; PRO0360; C2DOMAIN.
 DR PRINTS; PRO0390; PHPLIPASE.
 DR ProDom; PD001202; PI_PLC_Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00148; PLCX; 1.
 DR SMART; SM00149; PLCYC; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS00004; C2_DOMAIN_2; 1.
 DR PROSITE; PS00007; PIPLC_X_DOMAIN; 1.
 DR PROSITE; PS00008; PIPLC_Y_DOMAIN; 1.
 KW Hydrolyase; Lipid degradation; Transducer; Calcium-binding;
 KW Phosphorylation.
 FT DOMAIN 322 464 DOMAIN X.
 FT DOMAIN 542 652 DOMAIN Y.
 FT DOMAIN 661 765 C2 DOMAIN.
 FT CA_BIND 490 501 EF_HAND (POTENTIAL).
 FT ACT_SITE 337 337 BY SIMILARITY.
 FT ACT_SITE 382 382 BY SIMILARITY.
 FT MOD_RES 524 524 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 531 531 PHOSPHORYLATION (BY CAPK AND CGPK)
 FT (POTENTIAL).
 SQ SEQUENCE 801 AA; 91280 MW; DBAF8C829812DD9 CRC64;
 Query Match 18.0%; Score 600; DB 1; Length 801;
 Best Local Similarity 27.1%; Pred. No. 3.7e-31;
 Matches 167; Conservative 117; Mismatches 249; Indels 84; Gaps 18;
 QY 24 VFTIYS--ENERSARGELKFLHTEQGDVDTLDDAKIMERIRKDKWKSFGSLASINSD- 80
 DB 247 VFYKINGNGEWPIQGMDFRIEQSEV-WTEQCRLDIKKVHHE-----RLDC 295
 QY 81 LSKEARPKYLM-NPDLNGVLH-NVHQDMTPQMSHVFITGHSYLTGNQLSSDSDTFI 138
 DB 296 ISPFNEEFECGBANLAQYPTHTVTQDTSKPLSYFISSNHTYLSGHOLGLSSEMY 355
 QY 139 AALRRGVVRVVELDLPDDKGMKVTGNLTLPVSGFQKCVTAIKNAFTSPYPCVTI 198
 DB 356 TNLROGCKVELDVWDGNDGDIIFHGNLTLSQIKFHVCEIKARGETSPYPVILSL 415
 QY 199 EDHLTSELQHAALIEQLIGDALYPTPTDALVEFPSPESLKRKIIITKPKKEYLAC 258
 DB 416 EVCHSVQPMQIMANHMKFEIGML-PTPLPEGTKEPLTDLKLYKILLKGHTSHTVS 474
 QY 259 STOKLAMENLVLEEKEDKLEQTTFAPLEENHILGENTPSPRKEVEVLSQKEMSTPAE 318
 DB 475 GNSASSSSQSNITQDNDDD-----GAVDLTEYDE 504
 QY 319 LNSRPSDLGEATSTRYSKSDNDGNPKHFKYARLITIRLAKHAKGT--SMERHLQVDES 376
 DB 505 VDRSASSSSSSFSLSFGSSG-----KKKKITKIKIAPEFEELIYLVSHGFKSGNT 555
 QY 377 VKRI-----SLSEKLEKVEKWPALVKFTQKNLIRVPAANRVNSNFCPTLAWNYG 430
 DB 556 TREIPSYKIHSLVEEYKQLVQSEPREVVEASQNHLLRVYPRGTRFSDSSNDFMPMGWSIG 615
 QY 431 AQMAVNMOGYKELAQAFCKKGGCGGVLPKQVLLNLPSPGVFNFTSP-----RN 484
 DB 616 CQLAALNQQTSSPFWINDGFWSDNGCGVLPKPPCLLPG--ECETYDTPSPERIKSSY 673
 QY 485 TTLILKIKVMTTLGWDAFESKRFDLFSPPDFTRIVVGVPADEAKVTSVVDNS-WAP 543
 DB 674 SRLI--VNVISARQLPKYTKSTKGEVDP---VVTLSIVGTGHDQVKTKVIDNNGFNP 728
 QY 544 HWNEDEHFAKCEPALLRIEVRDHDSDKDEFEQGTCLPIHEVRDGYRCMQMDYKKNV 603
 DB 729 HWGEFEFFLYNSQLSMILLIRVDKDKVGHNRI-GHHCIRVENIRPGYRILKKNFNFT 787
 QY 604 LKGVLMFLHFQKCKCTF 620
 DB 788 IPLANLL-----CKFTF 799

RESULT 2
 PDI1_BOVIN
 ID PDI1_BOVIN STANDARD; PRT; 695 AA.
 AC P10895;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta 1
 DE (EC 3.1.4.11) (PLC-delta-1) (Phospholipase C-delta-1) (PLC-III)
 DE (Fragment).
 GN PLCD1.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 CC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88270495; PubMed=3390863;
 RA Suh P.-G., Ryu S.H., Moon K.H., Suh H.W., Rhee S.G.;
 FT "Cloning and sequence of multiple forms of phospholipase C.";
 RL Cell 54:161-169(1988).
 CC -!- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMES.
 CC -!- CATALYTIC ACTIVITY: 1-phosphatidyl-LD-myo-inositol 4,5-
 CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +
 CC diacylglycerol.
 CC -!- COFACTOR: REQUIRES CALCIUM.
 CC -!- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
 CC PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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 CC EMBL; M20638; AAA30710.1; -.
 DR PIR; C28821; C28821.
 DR HSSP; P10688; IMAI.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR000909; PI_PLC_X.
 DR InterPro; IPR001711; PI_PLC_Y.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00036; efhand; 2.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00388; PI-PLC-X; 1.
 DR Pfam; PF00387; PI-PLC-Y; 1.
 DR ProDom; PD001202; PI_PLC_Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00148; PLCX; 1.
 DR SMART; SM00149; PLCYC; 1.
 DR PROSITE; PS00018; EF_HAND; 2.
 DR PROSITE; PS00003; PH_DOMAIN; 1.
 DR PROSITE; PS00004; C2_DOMAIN_2; 1.
 DR PROSITE; PS00007; PIPLC_X_DOMAIN; 1.
 DR PROSITE; PS00008; PIPLC_Y_DOMAIN; 1.
 KW Hydrolyase; Lipid degradation; Transducer; Calcium-binding; Repeat.
 FT NON_TER 1 69
 FT DOMAIN <1 69
 FT CA_BIND 92 103 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 128 139 EF-HAND 2 (POTENTIAL).
 FT DOMAIN 235 379 DOMAIN X.


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DR PRINTS; PR00390; PHPLIPASEC.
DR PRODOM; PD001202; PI_PLC_Y; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00148; PLCX; 1.
DR SMART; SM00149; PLCYC; 1.
DR PROSITE; PS00018; EF_HAND; 2.
DR PROSITE; PS00003; PH_DOMAIN; 1.
DR PROSITE; PS00004; C2_DOMAIN; 2; 1.
DR PROSITE; PS00007; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS00008; PIPLC_Y_DOMAIN; 1.
KW Hydrolase; Lipid degradation; Transducer; Calcium-binding; Repeat;
KW 3D-structure.
FT DOMAIN 21 130 PH.
FT CA_BIND 153 164 EF_HAND 1 (POTENTIAL).
FT CA_BIND 189 200 EF_HAND 2 (POTENTIAL).
FT DOMAIN 296 440 DOMAIN X.
FT DOMAIN 492 609 DOMAIN Y.
FT DOMAIN 630 720 C2 DOMAIN.
FT ACT_SITE 311 311
FT ACT_SITE 356 356
SQ SEQUENCE 756 AA; 85962 MW; E33F2313AC81E9F9 Crc64;

Query Match 17.9%; Score 594.5; DB 1; Length 756;
Best Local Similarity 28.7%; Pred. No. 7.7e-31;
Matches 173; Conservative 96; Mismatches 215; Indels 119; Gaps 16;

QY 32 ERMSAEGLLKFLHTQGVDFDTLDDAKQIMERKDKKSKFGLASINDLSKEAFKRYLM 91
DB 226 ETLSEVERLVTFHQHOREEAGPALALSRIERYEPS-----ETAKAQRQMTKDFGLMYLL 280

QY 92 NFDLN--GVILNVQDHTQPMHSYFIETGHSYLTGNOLSSDSDTPIAALRGVRVV 149
DB 281 SADGNAFSLAHRRVYQDMDOPLSHVSSSHNTYLEDQLTGPPSTEAYIRALCKGCRCL 340

QY 150 ELDLPDDKGGMKVHGNLTNPVSFKQCVTAIKNNAFTSPYCVTIEDHLTSELOGH 209
DB 341 ELDCHWDPNQPEIYHYGTYFTSKILFCDVLRADYAFKASPPYVLSLENHCSLEQQRV 400

QY 210 AAELIQLGLDALYPPPTDVALVEFPSPSLKRLIIISTK-----PPK 252
DB 401 MARHLRAILGPILLDQPLDGVTTSLPSPQLKGLKILLKGLGILLPAGGENSGEATDVS 460

QY 253 EYLEACSTOKLAMENLVLEELEKEDKLEOTTFAPLEENHILGENTPSLRKEVEVLSQKE 312
DB 461 DEVERAEMEDAV--RSQVHKPKEDKLL-----VPEL-----492

QY 313 MSTPAELNSRSPDLGEATSTYKSDNGDNPKHFKYARLITIRLAKHAKTSMERLQ 372
DB 493 -----SDM-----IYCKS-----VHFG-----GFSSPGTSGQAFYE 519

QY 373 VDSVKRISISESKLEKVEKPEALVKFTOKNLRVYPAANRVNSNFCPTLAWNYGAO 432
DB 520 M-----ASFESRALRLQESNGFVRNVNCSLSRIYPAGWRTDSNYPVEMNGGQ 573

QY 433 MVAQNMQGKGKELQWQAFKFGKNGCGYVLPQYLLLENLPSPGVFNPTSPRNTLI 488
DB 574 IVALNQTPGPEVDVYLGCFQDNGCGYVLPKPAFLRD-----PNTTFNSRALTQGP 624

QY 489 -----LKKVWTTGLWDKAFKSRHDLFSPDPDFTRVIV--GVPADEAKWKTSVV-DN 539
DB 625 WWRPERLRVRIISQOOLPKV--NKNKNSIVDP-----KVIVEIHGVGRDTGSRQTAVITNN 678

QY 540 SWAPHNEDHEPALKPELALLRIEVRDHDSDSKDFEGOTCLPIHEVRDGYRCMOMYDK 599
DB 679 GFNPRMDMEFEFTVPDLALVRFWVEDYDSSKNDFIGOSTIPWNSLKGQYRHVLLSK 738

QY 600 KGN 602
DB 739 NGD 741
```

RESULT 4

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PID1_HUMAN STANDARD; PRT; 756 AA.
AC P51178;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta 1
DE (EC 3.1.4.11) (PLC-delta-1) (Phospholipase C-delta-1) (PLC-III).
GN PLCDL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RC MEDLINE=95197554; PubMed=7890667;
RA Cheng H.F., Jiang M.J., Chen C.L., Liu S.M., Wong L.P.,
RA Lomasney J.W., King K.;
RT "Cloning and identification of amino acid residues of human
RT phospholipase C delta 1 essential for catalysis.";
RL J. Biol. Chem. 270:5495-5505(1995)
CC -!- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
CC C ENZYMES.
CC -!- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +
CC diacylglycerol.
CC -!- COFACTOR: REQUIRES CALCIUM.
CC -!- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
CC PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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EMBL; U09117; AAA73567.1;
HSSP; P10688; IMAI.
MIM; 602142;
DR InterPro; IPR000008; C2.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001849; PH.
DR InterPro; IPR001192; PI_PLC_X.
DR InterPro; IPR000909; PI_PLC_Y.
DR InterPro; IPR001711; PI_PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00388; PI-PLC-X; 1.
DR Pfam; PF00387; PI-PLC-Y; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00390; PHPLIPASEC.
DR PRODOM; PD001202; PI_PLC_Y; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00148; PLCX; 1.
DR SMART; SM00149; PLCYC; 1.
DR PROSITE; PS00018; EF_HAND; 2.
DR PROSITE; PS00003; PH_DOMAIN; 1.
DR PROSITE; PS00004; C2_DOMAIN; 1.
DR PROSITE; PS00007; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS00008; PIPLC_Y_DOMAIN; 1.
KW Hydrolase; Lipid degradation; Transducer; Calcium-binding; Repeat.
FT DOMAIN 21 130
```

NCBI_TaxID=9913;
[L]
SEQUENCE FROM N.A.
TISSUE=Retina;
MEDLINE=93317620; PubMed=8327481;
Ferreira P.A., Shortridge R.D., Pak W.L.;
"Distinctive subtypes of bovine phospholipase C that have preferential
expression in the retina and high homology to the norpa gene product
of Drosophila";
Proc. Natl. Acad. Sci. U.S.A. 90:6042-6046(1993).
-!- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
DIACYLGlycerOL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
C ENZYMES. THIS FORM HAS A ROLE IN RETINA SIGNAL TRANSDUCTION.
-!- CATALYTIC ACTIVITY: 1-phosphatidyl-D-myo-inositol 4,5-
bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
diacylglycerol.
-!- COFACTOR: REQUIRES CALCIUM.
-!- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS; 1A, 1B (SHOWN HERE), 2A
AND 2B; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE RETINA.
-!- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN FOUR DIFFERENT FORMS
OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
-!- SIMILARITY: CONTAINS 1 C2 DOMAIN.

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or send an email to licenses@isb-sib.ch).

EMBL: L13936; AAA30699.1; -
EMBL: L13935; AAC37304.1; -
EMBL: L13937; AAA30700.1; -
EMBL: L13938; AAA30701.1; -
HSPG; P10688; IQAS.
InterPro: IPR000008; C2.
InterPro: IPR001192; PI_PL_C.
InterPro: IPR000090; PI_PL_C_X.
InterPro: IPR001711; PI_PL_C_Y.
Pfam: PF00168; C2; 1.
Pfam: PF00388; PI-PL-C-X; 1.
Pfam: PF00387; PI-PL-C-Y; 1.
PRINTS: PR00390; PHPFLIPASEC.
ProDom: PD001202; PI_PL_C_Y; 1.
SMART; SM00239; C2; 1.
SMART; SM00148; PLXCX; 1.
SMART; SM00149; PLCYC; 1.
PROSITE; PS50004; C2_DOMAIN_2; 1.
PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
Hydrolase; Lipid degradation; Transducer; Phosphorylation; Calcium;
Alternative splicing.
FT NON_TER 1
FT DOMAIN 149 299 DOMAIN X.
FT DOMAIN 413 529 DOMAIN Y.
FT DOMAIN 536 634 C2 DOMAIN.
FT ACT_SITE 164 164 BY SIMILARITY.
FT ACT_SITE 211 211 BY SIMILARITY.
FT VARSP_LIC <1 104 MISSING (IN ISOFORM 2A AND ISOFORM 2B).
FT VARSP_LIC 372 383 MISSING (IN ISOFORM 1A).
FT VARSP_LIC 372 383 MISSING (IN ISOFORM 2A).
FT SEQUENCE 1023 AA; 117109 MW; 416D700C2095748C CRC64;

Query Match 16.5% Score 549.5; DB 1; Length 1023;
Best Local Similarity 29.0%; Pred. No. 9.6e-28;
Matches 185; Conservative 104; Mismatches 231; Indels 119; Gaps 27;

30 ENRMSARGLLKFLHTEGD-----VDFTLDDAKIQMERIR-----KDWKKSFGLASINS 79
:: :: : | : | : | : | : ||| : | : | : | : | :

Db 69 KTYLTVQVLVFLNEHQRPRLNEILFPYDAKRAMQIEMEPDEDLKKQ-GL----- 122
 QY 80 DLSKEAPRYKLMNPDLNGVLHN--VVHODMTQPMQSHVFTGHNSYLTGNQLSSDSDTP 137
 Db 123 -ISSDGFVRLMSDENAPVFLDRLELYQEMDHLAYFTSSINTYLTGQFGCKSSVEM 181
 QY 138 IAAALRGVRVVDLWDPDKGMK---VTHGNTLNPVSKFCVTAIKNNAFFTSEYVPV 194
 Db 182 YRQVLLAGRCVVDLW- -DGKGEQDEPIITHGKAMCTDILFKVDVQAIKETAFTVSEYVPV 240
 QY 195 CVTIEDHLTSELQGHAAEILEILGALYPPPTDALVE-----FPSPESLKRKIII-- 246
 Db 241 ILSFENHCSYQYKMSKYCEDLFGDLLLQALESHPLEGRPLSPDLKRLIKLKQT 300
 QY 247 -STKPKEYLEACSTOKLAMENRNVELEKEDKLEQTTTFAPLEENHILGENTPPSLRKEV 305
 Db 301 TETEVEKKOLEALKSMMEAGESAAPVNMLEDDNE-----EET 337
 QY 306 EVLSQKEMSTPAEL--NSRSPSLG--EATSTRYSKSDG--NDNPK----- 346
 Db 338 ESAEQEEEAHPEYKYGNELSDADLGHKEATANSVKKASDDLEHNSKKGILVTVEDEQAWM 397
 QY 347 -HFKYARLIT-----IRLAKHAK-----GTSMEHRLQVDESVKRISLSEKLEKVE 392
 Db 398 ASKYVCATNTNIHPYLSLWNTNYAOPVKFGFVHAEERNHYNMS-----SFNSVGLGYLK 453
 QY 393 KWPEALVKTQKILNRYVPAANRVNSNFCPTLANNYGAQVMAQNNQGYGKELWQAFGR 452
 Db 454 THAIEFVNYNKRMSYRIPKGRVDSNYPQIFWNSGQVSLNYQTDPDLAMQLNQGRF 513
 QY 453 KNGGCGYVLPKYLENLPSPGVPNPTSPRNTTLILKIKVMTLW-----DKAFSKRHED 509
 Db 514 EYNSGCGYLLKPFMRPDRPTDFSET-PVGVTAATCSQVIGSQFLSDKKIGT----- 568
 QY 510 LFSPPDFTRVIVGVGPAD--EAKWKT-SVVDNSWAPHNWDEHFAK-----CPELALLRI 563
 Db 569 -----YVEVDYMGLEPTDIRKEPTRVMNGLNPVYNEE-SFVERKVLPLDLAVLRI 620
 QY 564 EYRDHDDSKDEFGTCLPIHEVRDGYRCMOMYDKGN 602
 Db 621 AV--YDDNNK--LIGORILPLDGLQAGYRHISLRN-EGN 654
 RESULT 6
 PTB4_HUMAN
 ID P1B4_HUMAN STANDARD; PRT: 1175 AA.
 AC Q15147; Q9J0J2; Q9BQW5; Q9BQW6; Q9BQW8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 4
 DE (EC 3.1.4.11) (PLC-beta-4) (Phospholipase C-beta-4).
 GN PLCB4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Retina;
 RX MEDLINE=96079091; PubMed=8530101;
 RA Alvarez R.A., Ghalavini A.J., Xu P., Hardcastle A., Bhattacharya S.,
 Rao P.N., Pettenati M.J., Anderson R.E., Baehr W.;
 RT "cDNA sequence and gene locus of the human retinal phosphoinositide-
 specific phospholipase-C beta 4 (PLCB4).";
 RL Genomics 29:53-61(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
 Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,
 Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
 Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,

RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 Clegg S., Copley V.E., Collier R.E., Connor R., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Levasiaho M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McElay K., McMurray A.A.,
 RA Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RL "The DNA sequence and comparative analysis of human chromosome 20.";
 Nature 414:865-871(2001).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
 MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 C ENZYMES. THIS FORM HAS A ROLE IN RETINA SIGNAL TRANSDUCTION.
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
 bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
 diacylglycerol
 CC -1- COFACTOR: REQUIRES CALCIUM.
 CC -1- ALTERNATIVE PRODUCTS: At least 3 isoforms; 1, 2 (shown here) and
 3; are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE RETINA.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN FOUR DIFFERENT FORMS
 OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -----
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 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AL031652; CAA21068.1; -
 DR EMBL; AL023805; CAC34525.1; -
 DR EMBL; AL023805; CAC34527.1; -
 DR EMBL; AL023805; CAC34528.1; -
 DR EMBL; L41349; AAB02027.1; -
 DR HSSP; P10688; IDJX.
 DR MIM; 600810; -
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR001192; PI-PLC.
 DR InterPro; IPR000909; PI-PLC_X.
 DR InterPro; IPR001711; PI-PLC_Y.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00388; PI-PLC-X; 1.
 DR Pfam; PF00387; PI-PLC-Y; 1.
 DR PRINTS; PR00390; PPHPLIPASEC.
 DR ProDom; PD001202; PI-PLC_Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00148; PLCXC; 1.
 DR SMART; SM00149; PLCYC; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
 DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
 DR Hydrolase; Lipid degradation; transducer; Phosphorylation; Calcium;
 KW Alternative splicing.
 KW DOMAIN 313 463 DOMAIN X.
 FT DOMAIN 565 681 DOMAIN Y.
 FT DOMAIN 688 786 C2 DOMAIN.
 FT ACT_SITE 328 328 BY SIMILARITY.

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FT CONFLICT 1057 1057 A -> V (IN REF. 3).
FT CONFLICT 1067 1067 L -> V (IN REF. 3).
FT CONFLICT 1084 1084 S -> C (IN REF. 3).
SQ SEQUENCE 1175 AA; 134496 MW; 7379C6BB95B8FCD CRC64;

Query Match 15.7%; Score 522.5; DB 1; Length 1175;
Best Local Similarity 28.0%; Pred. No. 6.5e-26;
Matches 180; Conservative 98; Mismatches 243; Indels 105; Gaps 26;

QY 30 ENERMSAEGLLKFLHTQGD-----VDFTLDDAK---QIMERIRKDWK-KSFGLASINSD 80
Db 233 KTDYTLVDQLVSLFNEHQDRPRLNEILFPFYDAKRAQIILEMYPDEELKKGL----- 286
QY 81 LSKAFKRYLMNPDNLGVNLN--VVHODMTQPMKSHYFIPTGHSYLTGNLSDDSDTPI 138
Db 287 ISSDGFRLMSDENAPVFLDRLELYQEMDHLAHYFISSSHNTYLTGRFGGKSSVEMY 346
QY 139 AALRRGVVRVVELDLPDDKGMK---VTHGNTLTNPVSPQKCTAIAKNNAFPTSEYVPC 195
Db 347 RQVLLAGRCVVELDCW-DGKEDEQEPITTHGKAMCTDILFKDVIQAKETAFYSEYVPI 405
QY 196 VTIEDHLSLTSELQHAAILQILGDALYPPPTDALVE-----PPSPESLKRKIIISTK-- 249
Db 406 LSFENHCKSYQOYQMSKYEDLFDGLLLKQALSHPLPGRLPLSPNDLKRKILIKNRL 465
QY 250 ---PPKEYLEACSTQKLAENRNVLVELEKEDKLEQTTFAPLEENHILGENTPSLRKEYE 306
Db 466 KPEVEKQLEALKSMFAGESAAPASILEDDNE-----EEIE 502
QY 307 VLSQKEMSTPAEL--NSRSPSDLG--EATSTRYSKS-----NGDNDNPKFKYARLIT--- 355
Db 503 SADQEEAHPKPYKFGNELSADDSFKHEAVANSVKGLVTVEDDQAMWASKYVGGATTNIH 562
QY 356 -----LRLAKHAK---GTSMEHRLQVDSVKRISLSKLEKVEKWEALVKETQKN 405
Db 563 PYLSTMLNVAQPKYFGFHVAAEERNIHYNMS-----SFNESPGLGYLTKTHAIEFVNYNKRO 618
QY 406 ILRYPAANRVSNFCPTLAWNYGAQMAQNMQGYGKELMQAFKFGKGGCGYVLLKQ 465
Db 619 MSRIYPKGGVRVDSNNYMPQIFWAGQMVSLNYQTPDLAMQNLQGFYNGSCGYLLKPD 678
QY 466 YLENLPSGVFPNPTSPRNTLLIKTKVMTTLGW---DKAFSKRHFDLSPDPFFTRVIV 522
Db 679 FMRRPRTDFPFSET-PVDGVIAATCSVOVISQFLSKDKIGT-----YVEVDM 726
QY 523 VGVPAD--EAKWKT-SVWDNSWAPHNEDHEFALK--CPELALLRIEVRDHDHDSKDEF 576
Db 727 YGLPTDTRKEFTRMVNNGLNPNVINEE-SFVFRKVIPLDLAVLRIAV--YDDNNK--L 781
QY 577 EGOTCLPIHEVRDGYRCMQMYKKGN 602
Db 782 IGQRILPLDGLQAGYRHSILRN-EGN 806

RESULT 9
P1PA_DROME STANDARD; PRT; 1095 AA.
AC P13217;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase
DE (EC 3.1.4.11) (Phosphoinositide-specific phospholipase C).
GN NORPA.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88311074; PubMed=2457447;

```

```

RA Bloomquist B.T., Shortridge R.D., Schneuwly S., Perdew M.H.,
RA Montell C., Steiller H., Rubin G., Pak W.D.;
RT *Isolation of a putative phospholipase C gene of Drosophila, norPA,
RT and its role in phototransduction.*;
RL Cell 54:723-733(1988).
CC !- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
CC C ENZYMES. NORPA IS INVOLVED IN PHOTOTRANSDUCTION.
CC !- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
CC diacylglycerol.
CC !- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
CC PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC !- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: J03138; AAA28724.1; -.
CC PIR: A31225; A31225.
CC HSP: F10888; IQAS.
CC FlyBase: FBgn0004625; norPA.
CC InterPro: IPR000008; C2.
CC InterPro: IPR001192; PI-PLC.
CC InterPro: IPR000909; PI-PLC_X.
CC InterPro: IPR001711; PI-PLC_Y.
CC Pfam: PF00168; C2; 1.
CC Pfam: PF00388; PI-PLC-X; 1.
CC Pfam: PF00387; PI-PLC-Y; 1.
CC PRINTS: PR00390; PHPLIPASEC.
CC ProDom: PD001202; PI-PLC_Y; 1.
CC SMART: SM00239; C2; 1.
CC SMART: SM00148; PLCX; 1.
CC SMART: SM00149; PLCYC; 1.
CC PROSITE: PS50004; C2_DOMAIN_2; 1.
CC PROSITE: PS50007; PIPLC_X_DOMAIN; 1.
CC PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
CC KW Hydrolase; Lipid degradation; Vision; Transducer.
CC FT DOMAIN 320 469 DOMAIN X.
CC FT DOMAIN 550 666 DOMAIN Y.
CC FT DOMAIN 673 771 C2 DOMAIN.
CC FT ACT_SITE 334 381 BY SIMILARITY.
CC FT ACT_SITE 381 381 BY SIMILARITY.
CC SQ SEQUENCE 1095 AA; 124822 MW; 2D945EF0ACBE69B3 CRC64;

Query Match 15.5%; Score 516.5; DB 1; Length 1095;
Best Local Similarity 28.0%; Pred. No. 1.4e-25;
Matches 178; Conservative 113; Mismatches 250; Indels 95; Gaps 27;

QY 12 PKGDPQLVGEVETIYSENER--MSAEGLLKFLHTQGD-----VDFTLDDAKQIMERI 64
Db 224 PRNDIE-----ELFTSITKQDFISLEQFIQFMNDKQDRPMNEILYPLYEKRCTEII 278
QY 65 R-----KDWKKSFGLASINSLSKAFKRYLMNPDNLGVNLN--V--HODMTQPMKSHYFI 117
Db 279 NDYELDEKK-----NVQMSLDGFKRYLMSDENAPVFLDRDLDFYEMDQPLAHYIN 331
QY 118 TGHNSYLTGNLSDDSDTPTAAALRGVRVVELDLPDDKGMK-----VTHGNTLTNPVS 174
Db 332 SSHNTYLSGRIGKSSVEMYRQTLLAGRCVVELDCW--NGKGEDEPIVTHGAYCTEIL 390
QY 175 FOKCVTAIKNNAFPTSEYVPCVTIEDHLSLTSELQHAAILQILGDALYPPPTDALVE- 233
Db 391 FKDCIQAIDACAFVSSEYVILSFENHCNRAQQYKLAQYCDDFDGLLLKLEPLDRPLDP 450
QY 234 ---FPSPELKRKIIISTKPPKEYLEACSTQKLAENRNVLVELEKEDKLEQTTFAPLEE 290

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Db	451	GLPLPPCKLRKRLIKRKRKPEVE-----KVELE-LWLKAGELTKDDDEEDA-----	498
Qy	291	NHILGENTPSLRKEVEVLSQKEMSTPAELNRSRPSDLG-----EATSTRYSKSDGNDNP	345
Db	499	-----SAGKPEAAAAAPAPAAAAAAGGAEGGGAAEAAAAAANSYSGTT-NVHP	548
Qy	346	---KHFKYARLITIRLAKHAGTSMERHL-QVDESVKRISLESKLEKVKVEKPEALVKF	401
Db	549	WLSSMVNTAQPTKQFGFKATEKNIHNNSSFAESAGMNYLKQSSID-----FVNY	599
Qy	402	TQKNLIRVYPAANRVNSNFCPTLAWNYGAQVAAQNMGGYKELWQAFKMGNGGCVY	461
Db	600	KRQMSRIYKPGTRADSSNIPQVFNAGCQMVSNLFSSDLPQLNGKKEFYNGGCGYL	659
Qy	462	LKQYLLLENLPSGVFNPTSPRNTTLIKIKVMTTLGWDKAFSRHEDLFSPPDPFFTRVI	521
Db	660	LKPDPMRADKDFDF-ADAPVDGVIAAQCCKVIAG--QFLSDKKVGYTYVEVDMF----	712
Qy	522	VGVPADEAK--WKTSVV-DNSWAPHNEDHEFALK---CPELALLRIEVRDHDSDSDE	575
Db	713	--GLPSTVVKKEFRTRLVANNGLNLYNED-PFVFRKVVLPDLAVLRFV--YBESGK--	765
Qy	576	REGQCLPIHEVRDGYRCMOMYDKKGNVKGVLMLF 611	
Db	766	ILQORILPLDGLQAGYRHVSL-RTEANFMSLPLMF 800	
RESULT 10			
PIP3_MOUSE			
Id	PIP3_MOUSE	STANDARD; PRT; 1234 AA.	
Ac	P51432.		
Dt	01-OCT-1996	(Rel. 34, Created)	
Dt	01-OCT-1996	(Rel. 34, Last sequence update)	
Dt	16-OCT-2001	(Rel. 40, Last annotation update)	
De	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 3		
De	(EC 3.1.4.11) (PLC-beta-3) (Phospholipase C-beta-3).		
Pl	PLCB3.		
Os	Mus musculus (Mouse).		
Oc	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Oc	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
Ox	NCBI_TaxID=10090;		
Rn	[1]		
Rp	SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.		
Rc	STRAIN=BAIB/C; TISSUE=Kidney;		
Rx	MEDLINE=98382438; Pubmed=9714794;		
Ra	Wang S., Zhou Y., Lukinius A., Oberg K., Skogseid B., Gobl A.;		
Rt	"Molecular cloning and characterization of a cDNA encoding mouse		
Rt	phospholipase C-beta3."		
Rl	Biochim. Biophys. Acta 1393:173-178(1998).		
Cc	!- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES		
Cc	DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS		
Cc	MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE		
Cc	C ENZYMES.		
Cc	!- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-		
Cc	bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +		
Cc	diacylglycerol.		
Cc	!- COFACTOR: REQUIRES CALCIUM (BY SIMILARITY).		
Cc	!- SUBCELLULAR LOCATION: Nuclear.		
Cc	!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN KIDNEY, SKELETAL MUSCLE,		
Cc	LIVER, LUNG, HEART AND BRAIN.		
Cc	!- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS		
Cc	OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.		
Cc	!- SIMILARITY: CONTAINS 1 C2 DOMAIN.		
Cc	-----		
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Cc	between the Swiss Institute of Bioinformatics and the EMBL outstation.		
Cc	the European Bioinformatics Institute. There are no restrictions on its		
Cc	use by non-profit institutions as long as its content is in no way		
Cc	modified and this statement is not removed. Usage by and for commercial		
Cc	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
Cc	or send an email to license@isb-sib.ch).		
Cc	-----		
Query Match 15.2%; Score 506.5; DB 1; Length 1234;			
Best Local Similarity 27.4%; Pred. No. 7.5e-25;			
Matches 174; Conservative 102; Mismatches 239; Indels 119; Gaps 24;			
Qy	34	MSAEGLLKFLHTEQGDVDF-----LDDAKQIMERIKDKWKSFGLA 75	
Db	241	LTLQLMDFINQKQRPRLNEVLPPLRSQARLLIEKYETNKQFLER-----	288
Qy	76	SINDLSKEAFKRYLMPDLNGVLHV---VHODMTPKSHYFIFGHSYLTGNOLSSD 132	
Db	289	---DQMSMEGFSRYLGEE--NGILPLEALDLSMDMTQPLSAYFINSHNYLTAGQLGP 344	
Qy	133	SSDPTPIAAALRRGVVVELDLW----PDRKGGMKTHGNTLTNPVSFOKCVTAIKNAFF 188	
Db	345	SSVEMYQALLNGRCVELDWKGRPEEE--PFITHGFTMTTEVPLRDVLEAIAEAAFK 402	
Qy	189	TSEYPVCVTIEDHLTS--ELQGHAAEILEQILGALYPP-----TTDALVEFPSPESIKRK 243	
Db	403	TSPYVILSFENHVDSAKQAQAKAAYCYSIFGDALLIDPLDKYPLSAGIPPLSPQDLNMR 462	
Qy	244	IIISTKP---PKEYLEACSTQKLAENRNLVEELEKEDKLEQTTFAPLEENHILG----E 296	
Db	463	ILVANKKRRHPSGTGVPDSSVKKRPLEQSN-----SALSSESAATEPSSPOLGSPSSD 514	
Qy	297	NTPSLRKEVEVLSQK-----EMSTPAELNRSRPS-----DLGEATSTRYS 336	
Db	515	SCPGLSNGEEVGLKTSLEPQKSLGEESLSREPVPMPDRDRDEDEDEDEETTPPKP 574	
Qy	337	KSNDGNONPKHFYARLIT--IRLAKHAKGSMERHLQVDSVKRISLESKLEKVVVEKWP 395	
Db	575	TTDEGTASSEVNATEEMSTLVNVEYVVKFSFEASRRKNCFCFEMSSFEVETKAMEQLTKSP 634	
Qy	396	EALVKFTQKNLIRVYPAANRVNSNFCPTLAWNYGAQVAAQNMGGYKELWQAFKMGKGN 455	
Db	635	MEFVEYNKQQLSRIYKPGTRVDSNNYMPQLFWNVGCOLVALNFQTLDLPLQMLNAGVFEYN 694	
Qy	456	GGCGYVLKQVLLLENLPSGVFNPTSPRNTLI-----LTKVMTTLGWDKAFSKRH 507	
Db	695	GRSGYLLKPEFMRPRDKSDFP-----TEVIVDGVIVANALRVKVIS----GQFLSDKK 743	
Qy	508	FDLSPDPFFTRVIVGVVPAD--EAKWKTSSVVD--NSWAPHNED--HEF--ALKCPCLALLRI 563	
Db	744	VGIVVEVDMF-----GLPVDTRKRYTRISQGSFNPVWDEEFDFFPKVVLPLASLRI 797	
Qy	564	EVROHDDSDSKDFEQGTCLPIHEVRDGYR--CMQ 595	

798 AAFEEG----GKFGHRLPVSAIRSGYHYVCLR 827

Db 798 AAFEEG----GKFGHRLPVSAIRSGYHYVCLR 827

RESULT 11

PIBL_BOVIN STANDARD; PRT; 1216 AA.

AC P10894;

DT 01-JUL-1989 (Rel. 11, Created)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 1 (PLC-beta-1) (PLC-154).

DE (EC 3.1.4.11) (PLC-beta-1) (Phospholipase C-beta-1) (PLC-154).

GN PLCB1.

OS Bos taurus (Bovine).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE=88270496; PubMed=2455601;

RA Katan M., Kriz R.W., Totty N., Philip R., Meldrum E., Aldape R.A.,

RA Knopf J.L., Parker P.J.;

RT "determination of the primary structure of PLC-154 demonstrates

RT diversity of phosphoinositide-specific phospholipase C activities.";

RL Cell 54:171-177(1988).

CC -! FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES

CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS

CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE

CC C ENZYMES.

CC -! CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-

CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +

CC diacylglycerol.

CC -! COFACTOR: REQUIRES CALCIUM.

CC -! MISCELLANEOUS: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-BETA 1 IS

CC MEDIATED BY TWO G-PROTEIN ALPHA SUBUNITS, ALPHA-O AND ALPHA-11.

CC -! SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS

CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.

CC -! SIMILARITY: CONTAINS 1 C2 DOMAIN.

CC

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CC or send an email to license@isb-sib.ch.

CC -----

CC EMBL; J03137; AAA30702.1; -

CC PIR; A28822; A28822.

CC HSSP; P10688; IDJX.

CC InterPro; IPR000008; C2.

CC InterPro; IPR001192; PI_PLC.

CC InterPro; IPR000909; PI_PLC.X.

CC InterPro; IPR001711; PI_PLC.Y.

CC Pfam; PF00168; C2; 1.

CC Pfam; PF00388; PI_PLC-X; 1.

CC Pfam; PF00387; PI_PLC-Y; 1.

CC PRINTS; PR00390; PHPLIPASEC.

CC ProDom; PD001202; PI_PLC_Y; 1.

CC SMART; SM00239; C2; 1.

CC SMART; SM00148; PLCXc; 1.

CC SMART; SM00149; PLCYc; 1.

CC PROSITE; PS50004; C2_DOMAIN_2; 1.

CC PROSITE; PS50007; PIPLC_X_DOMAIN; 1.

CC PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.

CC Hydrolase; Lipid degradation; Transducer; Phosphorylation; Calcium.

CC KW DOMAIN 316 467

CC FT DOMAIN 540 656

CC FT DOMAIN 663 761

CC FT DOMAIN 331 331

CC ACT_SITE 378 378

CC ACT_SITE 378 378

CC MOD_RES 887

CC BY SIMILARITY.

CC PHOSPHORYLATION (BY PKC).

CC

SQ SEQUENCE 1216 AA; 138714 MW; BEF809177F1B7ABB CRC64;

Query Match 15.2%; Score 504.5; DB 1; Length 1216;

Best Local Similarity 26.3%; Pred. NO. 9.9e-25;

Matches 179; Conservative 111; Mismatches 263; Indels 127; Gaps 25;

QY 2 CSIAACRSGTPKGPEDQDLVGEVFTIYSEN-----ERMSAEGLKF 42

DB 192 CSLPSSRNDSS---IPQEDFTPEYRVLNLCRPEIDNIFSEFGAKSPYLVDMDF 248

QY 43 LHTQGD-----VDFTLDDAKQIMERKDWKSGFGLASINDSLKEAFKRYLMPDLNG 97

DB 249 INLKORDPLNEILYPLKQEQOVLTLEK-YEPNNSLAK-KGOISVDGFMRYLSEEN-NG 305

QY 98 VLHNV---VHDMQPMKSHYFIFGTGNSYLTGNLSDSDSDTPIAAALRRGVVYVELDLM 154

DB 306 VVSEPKLDLNMDSQPLSHYFINSNHTYITAGQLAGNSSVEMYRQVLLSGRCVCLDCW 365

QY 155 PDDKGMK-----VTHGNTLTNPVSFOKCVTAIKNNAFFTSEYPCVCTIEDHLTS-ELQG 208

DB 366 ---KGTAEPEPVITHGFTMTTEISFKEVIEAIEACAFKTSPPILLSPFNHVDSPKQA 422

QY 209 HAAEILQILGALYYP-----TTDALVEFPSPESLAKKIIISTKPKP-EYLEACSTQKL 263

DB 423 KMAEYCRILFGDALLMEPLDKYPLESGVPLPSPMDLMYKLVKNKKSHKSSGSGKKL 482

QY 264 AMENRNVLVELEKEDKLEOTTPAPLEENHILGENTPSPURKEVEVLSKEMSTP-----AEL 319

DB 483 SEQATNYSYD-----SSSVFEP-----SSPGAGEADT 509

QY 320 NSRSPDLGENTSTRYKSNQDNDNPKHFKYARLITIRLAKHAKGTSMEHRLQVDESVR 379

DB 510 ESDDDDDDCKKSDMDGEGTAGSEAMATEESNL--VNYIQPVAFESFEISKRRSFEM 567

QY 380 ISLESLEKLVKWEKPEALVKFTQKNILVYPAANRVSSNFCPTLANNYGAQVANOQ 439

DB 568 SSFVETKLEQLTKSPVEFVEYKMKLSRIYKPTRVDSNTPQLFWNACQWALNFQ 627

QY 440 GYKELMQATGKFGNGCGYVLKPOYL-----LENLPSPGPPFPNTPSPRNTTIL 489

DB 628 TVDLAMQINMGWYENYKSGYRLKPEMRPDKHDFPTEGIVDGVAN-----TSLV 680

QY 490 KIKVMTTLGMDKAFSKRHFDLSPDPFFTRVIVGVPADEA---KWKTSVVDNSWAPHW 545

DB 681 KLIISQFLSDKKVGYVEVDMF-----GLPVDTRRAKFKTKTS-OGNAVNFIV 727

QY 546 NEDHEFALK--CPELALLRIEVRDHDSDSKDEFGOTCLPIHEVRDGYRCMQMDYKKNV 603

DB 728 EEEPIVFKKVVPLSLACLRIAV--YEEGK--FIGHRLFPVQAIRPGYHYICLRNERNOP 783

QY 604 LKGVLMFLHFQCKCKTQDFT 623

DB 784 LM-LPALFYIEVKDYVDPDT 802

RESULT 12

PIBL_HUMAN STANDARD; PRT; 1216 AA.

ID P1B1_HUMAN

AC Q9NQ66; Q9NQ65; Q9NQH9; Q9NTH4; O60325; Q9H4H2; Q9BQW2; Q9UJF6;

AC Q9UM26;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 1 (PLC-beta-1) (PLC-beta-1) (Phospholipase C-beta-1) (PLC-154).

DE (EC 3.1.4.11) (PLC-beta-1) (Phospholipase C-beta-1) (PLC-154).

GN PLCB1 OR KIAA0581.

OS Homo sapiens (human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS A AND B).

[illegible]

Qy	98	VLHNV----	VHODMTQPMGHYFIFTHGNSYLTGNLSDDSDTPTAAALRRGVVVVELDW	154
Db	306	VVSPEKLDLNEDMSOPLSHYFINSHTYLTAGLAGNCSVEMYRQVLLSGCRCEVDCW	365	
Qy	155	PDDKGGMK-----	VTHGNLTNPVSPKCVTAIKNNAFFTSEYPCVCTHIEDHLTS--ELQG	208
Db	366	---KGRTAEEPVTGHGFTWTTETISFREVTEATAECAFKTSPFPILLSPFNHVDSPKQQA	422	
Qy	209	HAAATEILOIGDALYYP-----	TWDALVEFPSPESLKRKIIISTKPKPKYLEACSTQKLA	264
Db	423	KMAEYCRLIIFGDALLMPELKEYPLESGVPLSPMDLMIYLVKNK-----	467	
Qy	265	MENRNLVEELEKEDKELEQTTFAPLEENHILGENTPSLKRVEVLSOKEMSTPAELNSR--S'	323	
Db	468	-----	KSKHSESGRKK-----LSEQASNTYSDSSMFE	498
Qy	324	PSDLGEATSTRYKSNDDGNDNPKHFY-----	ARLIT-----IRLAKHAKGTSMGHR	370
Db	499	PSSPGAGEADTESDDDDDDDDCKSSMDECTAGSEAMATEEMSNLVNYIQPVKFPSPIS	558	
Qy	371	LQVDESVKRISLSSEKLEKVVKEWPEALVKFTQKNILRVYPAANRVNSNFCPTLAWNYG	430	
Db	559	KKRKSEFEMSFFVETKLEOLTQSPVEFYENKMQLSRIYPKRGTRVDSNMTQPLFWNAG	618	
Qy	431	AQWVAONMOGYKELMAQFAEKFKNGCGCYVLKPOVL-----	LENLPSGVFPNPT	480
Db	619	COMVALNFQMDLAWQINMGWEYNGKSGYRLKPFEMRRPKDHPDFTTEGIVDGVAN--	676	
Qy	481	SPRNTLILIKVYTWTLGWDKAFSRKHFDLPSPDPFFTRVIVGVPADEA-----	KWKTSV	536
Db	677	-----	TLSVKILTSQGFLSDKKYGVTVYEDMF-----GLPVDTRRKAFTKTS-	718
Qy	537	VDNSWAPHNNEDEFALK--	CPELALLRLEVREDHDDSKDFEGOTCLPIHEVRDGYRCM	594
Db	719	QGNAPVNPWEEEPVPFKVVLFTLACLRIV--	VEEGK--FIGHRILPVQAIRPGHYI	774
Qy	595	QMTDKKGNVL	604	
Db	775	CLRNERNOPL	784	

RESULT 13

PIBL_RAT 1
ID AC PIIBL_RAT STANDARD; PRT; 1216 AA.
AD P10687;
01-JUL-1989 (Rel. 11, Created)
DT DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT DT 16-OCT-2001 (Rel. 46, Last annotation update)
DE DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 1
DE DE (EC 3.1.4.11) (PLC-beta-1) (phospholipase C-beta-1) (PLC-154) (PLC-154).
GN PLCB1.
OC Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88270495; PubMed=3390863;
RA Suh P.-G., Ryu S.H., Moon K.H., Suh H.W., Rhee S.G.;
RT "Cloning and sequence of multiple forms of phospholipase C.;"
RL Cell 54:161-169(1988).
CC -! FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
CC C ENZYMES.
CC -! CATALYTIC ACTIVITY: 1-phosphatidyl-ld-myo-inositol 4,5-
CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
CC diacylglycerol.
CC -! COFACTOR: REQUIRES CALCIUM.
CC -! MISCELLANEOUS: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-BETA 1 IS
CC MEDIATED BY TWO G-PROTEIN ALPHA SUBUNITS, ALPHA-Q AND ALPHA-11.
CC -! SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS

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OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
-!- SIMILARITY: CONTAINS 1 C2 DOMAIN.

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or send an email to license@isb-sib.ch.

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EMBL; M20636; AAA41885.1; -.
PIR; A28821; A28821.
HSP; P10688; 1DJX.
InterPro: IPR000008; C2.
InterPro: IPR001192; PI_PLC.
InterPro: IPR000909; PI_PLC_X.
InterPro: IPR001711; PI_PLC_Y.
Pfam; PF001568; C2; 1.
Pfam; PF00388; PI-PLC-X; 1.
Pfam; PF00387; PI-PLC-Y; 1.
PRINTS; PR00390; PHILIPASEC.
ProDom; PD001202; PI_PLC_Y; 1.
SMART; SM00239; C2; 1.
SMART; SM00148; PLCxc; 1.
SMART; SM00149; PLCyc; 1.
PROSITE; PS50004; C2_DOMAIN_2; 1.
PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
Hydrolase; Lipid degradation; Transducer; Phosphorylation; Calcium.
DOMAIN 316 467
DOMAIN 540 656
DOMAIN 663 761
ACT_SITE 331 331
ACT_SITE 378 378
MOD_RES 887 887
SEQUENCE 1216 AA: 138344 MW: 92P23691781F788F C9264.

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Query Match 15.0%; Score 499; DB 1; Length 1216;
Best Local Similarity 26.0%; Pred. No. 2.2e-34;
Matches 172; Conservative 110; Mismatches 253; Indels 126; Gaps 24;

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QY 2 CSIACSGTPKGPDEQDLVGEFTIYSEN-----ERMSAEGLLKF 42
Db 192 CSLSPSRNDS---IPQEDFTPDYRVFLNNLCRPRPEIDNIFSEFGAKSPYITVQOMDMF 248
QY 43 LHTQGD-----VDFTLDDAKAWERIRKDWKSGFLASINSDSKAEAPRYLIMPDLNG 97
Db 249 INLKORDPRLNEILYPLKOEQOVQVLEK-YEPNSSLAK-KGQMSVDGFMRYLSGEE-NG 305
QY 98 VLNHV---VHODMTQPMASHYFIETHGNSYLTGNOLSSDSDPTIAALRRGVVVELDLM 154
Db 306 VVSPKLDLNMDSQPLUSHFIINSHTYLTAGLAGNSSVEMYQVLLSGRCRVELDCW 365
QY 155 PDDKGMK-----VTGNTLTNPVSQKCVATAKNNAFPTSPYPCVCTIEDHLTS-ELQG 208
Db 366 ---KGRTAABEPVITHGFTWTTETSPKEVIEALAECAFTSPFPILLSEFHVDSPKQQA 422
QY 209 HAAEILEQILGDALYYP-----TTDALVFEPSPESIKRKIIISTKPKK-EYLEACSTOKL 263
Db 423 KMAEYCRLLIFGDALLMEPLEKYPLESGVPLPSPMDLMTYKLVKNKKSHKSSGSGKKKL 482
QY 264 AMENRNLVLEELEDKLEOTTFAPLEENHILGENTPSLRKEVEVLSQEMSTP-----AEL 319
Db 483 SEQASNTYS-----SSSVPEP-----SSPGAGEADT 509
QY 320 NSRSPDLGEASTRYSKNSDGNNDNPKFKYARLITIRLAKHAKGTSMEHRLQVDESVKR 379
Db 510 ESDDDDDDDCKKSSMDGECTAGSEAMATEEKSNL-VVYIQPVKESFEFSKRNKSFEM 567
QY 380 ISLSESKLEKVEKWEALVFTQKNILRVYPAANRVNSSNFCPTLAWNYGAQMVAQNMQ 439
Db 510 ISLSESKLEKVEKWEALVFTQKNILRVYPAANRVNSSNFCPTLAWNYGAQMVAQNMQ 439

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Db	568	SSFVETKGLBQLTKSPVEFYENKMQLSRIYPKGRVDSNYPQLFWNNACQWALNTQ	621
QY	440	GYGKELMQAFGKFGNGCGGYVLKPOYL-----LENLPSCGVFPNFTSPRNTTLIL	489
Db	628	TVDLAMQINMGVYENKSGYRLKPEFMRRDPKHDPFTFEGIVGAN-----TLSV	680
QY	490	KIKVMTTLGWMDKAFSKRHFLDSPDPFFTRVIVGVPADEA---KWKTSVDNSNAPHW	545
Db	681	KIISQFSLDRKVGTYVYEVDMF-----GLPVDTRKQAFKTKIS-QGNANVPW	727
QY	546	NEDHEFALK--CPALALLRIEVRDHDHDDSKDFEQTCPLPIHEVRDGYRCMQMYDKKGV	603
Db	728	EEPIPVFKKVLPSLACLRFAA--YEEGCK--FIGHRIPLVQAIRPGVHYICLRNERNOP	783
QY	604	L 604	
Db	784	L 784	

RESULT	14
PIP3_HUMAN	
ID	PIP3_HUMAN
AC	Q01970;
CD	STANDARD;
PT	PRT;
NC	1234 AA.
DT	01-JUL-1993 (Rel. 26, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 3
DE	(EC 3.1.4.11) (PLC-beta-3) (Phospholipase C-beta-3).
GN	PLCB3.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RI	[1]
SE	SEQUENCE FROM N.A.
RX	MEDLINE=95336441; PubMed=7612006;
RA	Laquerantz J., Schoen T.J., Chader G.J., Rodriguez I.R.;
RT	"Structural organization and expression of the human
RT	phosphatidylinositol-specific phospholipase C beta-3 gene.;"
RL	Biochem. Biophys. Res. Commun. 212:190-195(1995).
RL	[2]
SE	SEQUENCE FROM N.A.
RX	MEDLINE=95331781; PubMed=7607669;
RA	Laquerantz J., Carlson E., Phelan C., Grimmond S., Rosen A.,
RA	Dare E., Nordenskjold M., Hayward N.K., Larsson C., Weber G.;
RT	"Genomic organization and complete cDNA sequence of the human
RT	phosphoinositide-specific phospholipase C beta 3 gene (PLCB3).;"
RL	Genomics 26:467-472(1995).
RL	[3]
SE	SEQUENCE OF 184-1234 FROM N.A.
RX	MEDLINE=93092988; PubMed=1333955;
RA	Carozzi A.J., Kriz R.W., Webster C., Parker P.J.;
RT	"Identification, purification and characterization of a novel
RT	phosphatidylinositol-specific phospholipase C, a third member of the
RT	beta subfamily.;"
RL	Eur. J. Biochem. 210:521-529(1992).
RL	[4]
SE	SEQUENCE OF 184-1234 FROM N.A.
RA	Merberg D.M.;
RL	Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
CC	-1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
CC	DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
CC	MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPAS
CC	C ENZYMES.
CC	-1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
CC	bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +
CC	diacylglycerol.
CC	-1- COFACTOR: REQUIRES CALCIUM.
CC	-1- SUBCELLULAR LOCATION: Membrane-bound.
CC	-1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
CC	OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC	-1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC	-----

RESULT	15
ID	PLC1_SCHPO
STANDARD;	PRT; 899 AA.
PLC1_SCHPO	
P40977;	
01-FEB-1995	(Rel. 31, Created)
01-FEB-1995	(Rel. 31, Last sequence update)
16-OCT-2001	(Rel. 40, Last annotation update)
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase 1	
(SC 3.1.4.11) (PLC-1) (Phospholipase C-1).	
PLC1 OR SPAC22F8.11.	
Schizosaccharomyces pombe (Fission yeast).	
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;	
Schizosaccharomycetales; Schizosaccharomycetaceae;	
Schizosaccharomycetes.	
NCHI_TaxID=4896;	
[1]	
SEQUENCE FROM N.A.	
MEDLINE=95250375; PubMed=7732727;	
Andoh T., Yoko-O T., Matsui Y., Toh-E A.;	
"Molecular cloning of the plc1+ gene of Schizosaccharomyces pombe,	
which encodes a putative phosphoinositide-specific phospholipase C.";	
Yeast 11:179-185(1995).	
[2]	
SEQUENCE FROM N.A.	
STRAIN=972;	
MEDLINE=96020169; PubMed=8590474.	

Query Match

Query Match 14.38; Score 476; DB 1; Length 899;
Best Local Similarity: 25.08

Sequence similarity 20.0%; pred. No. 4.3e-23;
Matches 163; Conservative 94; Mismatches 231; Indels 138; Gaps 23;

Qy	23	EVFTIYSE----	NERMSAEGLLKFLHTEQGDVDF	TLDDAKQIMERIRDKWKSEGLASIN	78
		I: I: I	: : : I I I	I	
Db	367	EIVDFKEYTSGDKMSLEQFRHFLSTQ	-----	KARLDSDSIRTLVVSFCS	413
				I: I : : :	

79 SDLSKEA---FRKYLMPDLNGVLHN---VVHQDMTPMSHYFIETGHNLSYLTGNQLSS 131

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Sun Jul 28 10:34:37 2002

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Db 414 NDDSKMGLIEFTSLSP-----HNSPVVPIQDMSPRLNEYLISSSHNTYLLGKQFGG 467
Qy 132 DSSDTPIAAALRRGVVVELDLPDDKGMKVTHGNTLTNPVSFKQCVTAIKNNAFTSE 191
Db 468 ESSIEGYIRSLQRCCKCIEIDCW-DGPNPVPVCHGHTFTSMIKENDVIDAIRKYAFVSP 526
Qy 192 YPVCVTIEDHLTSELQGHAAETLEILGDALYYPPTTDALVEFPSPESLKRKIIISTKPP 251
Db 527 YPLFTISLEIHCPCDQORQOMVSMKQAFGDTLVKRPVTANESVLPSPEDLLNKILLKVK-- 584
Qy 252 KEYLEACSTOKLAMENRNIVELEKEDEKLEQTFAPLEENHILGENTPSLKEVEVLSQK 311
Db 585 -----CSATPLHOFSTDILKVGITDSDTTESSELENSLTG-----LRK-----GKR 628
Qy 312 EMST--PAELNSRSPDLGEATSTRYKSNDCNDNPKHFKYARLITIRLAKHAKGTSMEH 369
Db 629 RMKNIIVQELQQLAP-----YARSLKFR-----651
Qy 370 RLQVDESVKRISLESKL-----EKVVEKWPEALV-----KFTQKNILRVYPAANRYN 417
Db 652 -----NFSLPESKTYSHIFSERTIKKHGKAMVPRLSKHNLRYLCRVYPGPLRVG 702
Qy 418 SSNFCPTLAWNYQAQWVAQNMQYKELWQAFCKFKGNGCGVYLPK--OYLL-----E 469
Db 703 STNFPQVYWRGLGVQVVALNMQTYDTGLQINDALFTADPTGYLLKPPCQRIIGTVGEE 762
Qy 470 NLPSGVFPNTPSPRNTTILIKIKVMTTLGWDKAFSKRHFDLFSPPDFTTRVIVGVPADE 529
Db 763 GLPRKIK-----LTIDVISQQLRRARELSNSETLSP---YVEIQVHSMEEESP 807
Qy 530 AKWTSVY-DNSWAPHWNED--HEFALKCPELALLRIEVRDHDHDDSKDE-FEGOTCLPIH 585
Db 808 FRWCSKVVHENGFRFPFNGETMVYESIISDDFYSMIRFLVHHRGNSGNDISIFANFTC-PID 866
Qy 586 EVRDGYRCMQMYDKKG-NVLKGVLM 610
Db 867 RLQOGYRHIRLDMQGENLFFSLFL 892

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Job time: 382 sec